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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:27:20 ; Search time 52 Seconds

(without alignments)
43.469 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gffselw 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 121633

Minimum DB seq length: 11

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	46	100.0	12	4	AAB86005 DCM-asso
2	46	100.0	13	4	AAB86006 DCM-asso
3	46	100.0	14	4	AAB86012 DCM-asso
4	46	100.0	14	4	AAB86020 DCM auto
5	46	100.0	15	4	AAB86013 DCM-asso
6	46	100.0	15	4	AAB86021 DCM auto
7	30	65.2	13	4	AAB86009 DCM-asso
8	30	65.2	13	4	AAB86007 DCM-asso
9	30	65.2	13	5	AAW47221 Dilated c
10	30	65.2	15	4	AAB86028 DCM auto
11	30	65.2	15	4	AAB86017 DCM-asso
12	30	65.2	15	4	AAB86014 DCM-asso
13	30	65.2	15	4	AAB86022 DCM auto
14	30	65.2	15	5	AAO20307 Human ple
15	29	63.0	15	6	AAU37231 Rhodopsin
16	27	58.7	11	2	AAW11231 Peptide A
17	27	58.7	11	4	AAU27152 Human Leu
18	27	58.7	11	4	AAU26842 Human Leu
19	27	58.7	11	5	AAW52269 Miniature
20	27	58.7	12	2	AAW37181 Human p53
21	27	58.7	12	2	AAW37188 Human onc
22	27	58.7	12	2	AAW37189 Human onc
23	27	58.7	12	3	AAW17076 Mdm/hdm a
24	27	58.7	12	3	AAW17087 Mdm/hdm a
25	27	58.7	12	3	AAW17088 Mdm/hdm a

26	27	58.7	12	3	AAB17075 Mdm/hdm a
27	27	58.7	12	5	ABB73170 Mdm/hdm a
28	27	58.7	12	5	ABB73183 Mdm/hdm a
29	27	58.7	12	5	ABB73171 Mdm/hdm a
30	27	58.7	12	5	ABB73182 Mdm/hdm a
31	27	58.7	13	3	AAV57799 TRAM-inte
32	27	58.7	14	5	ABB05528 Biotinyla
33	27	58.7	15	2	AAB054909 Immunodom
34	27	58.7	15	2	AAR54910 Immunodom
35	27	58.7	15	2	AAR89914 p53 prote
36	27	58.7	15	2	AAV06310 Human p53
37	27	58.7	15	3	AAV99001 HLA class
38	27	58.7	15	3	AAB22780 Human amy
39	27	58.7	15	3	AAB29161 Peptide #
40	27	58.7	15	3	AAB29159 Peptide #
41	27	58.7	15	3	AAB29167 Peptide #
42	27	58.7	15	3	AAB29160 Peptide #
43	27	58.7	15	3	AAB29157 Peptide #
44	27	58.7	15	4	AAG89730 p53 DR3 b
45	27	58.7	15	4	AAG89500 p53 DR 3a

ALIGNMENTS

RESULT 1
AAB86005
ID AAB86005 standard; peptide; 12 AA.

XX AAB86005;

DT 12-JUL-2001 (first entry)

XX DCM-associated peptide #5.

XX DCM; dilatative cardiomyopathy; autoantibody; cardiant;

KW beta-1 adrenergic activated antibody; immunosuppressive.

XX Synthetic.

OS WO200121660-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-EP009241.

XX 21-SEP-1999; 99EP-00118630.

XX 21-SEP-1999; 99EP-00118631.

XX 'AFFI-' AFFINA IMMUNTECHNIK GMBH.

XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX WPI; 2001-335469/35.

XX New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.

XX (Claim 3, Page 20; 29pp; German.

XX This invention describes a novel peptide (P1) which can be used for (1)

CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid

CC phase; and (2) a chromatographic apparatus with (P1) bound. the products

CC of the invention have cardiant and immunosuppressive activity. (P1) is

CC used to produce medicine to combat beta 1 adrenergic activated

CC autoantibodies having a causal pathological relationship with dilatative

CC cardiomyopathy. This sequence represents a specifically claimed peptide

CC used to illustrate the method of the invention

XX Sequence 12 AA;

XX Query Match 100.0%; Score 46; DB 4; Length 12;

XX Best Local Similarity 100.0%; Pred. No. 0.064;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
 |||||
 Db 2 GSFFSELM 9

RESULT 2
 AAB86006
 ID AAB86006 standard; peptide; 13 AA.
 XX
 AC AAB86006;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM-associated peptide #6.
 XX
 XX DCM; dilative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.
 XX
 OS Synthetic.
 XX
 PN WO200121660-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-EP009241.
 XX
 PR 21-SEP-1999; 99EP-00118630.
 PR 21-SEP-1999; 99EP-00118631.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX
 DR WPI; 2001-335469/35.
 XX
 XX New peptide useful for combating the autoantibodies that are responsible
 PT for dilative cardiomyopathy.
 XX
 PS Claim 3; Page 21; 29pp; German.
 XX
 CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta 1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 46; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
 |||||
 Db 3 GSFFSELM 10

RESULT 3
 AAB86012
 ID AAB86012 standard; peptide; 14 AA.
 XX
 AC AAB86012;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM-associated peptide #12.
 XX
 KW DCM; dilative cardiomyopathy; autoantibody; cardiant;

KW beta-1 adrenergic activated antibody; immunosuppressive.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 14
 FT /note= "Lys modified with an amide or free acid group"
 FT

XX
 PN WO200121660-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-EP009241.
 XX
 PR 21-SEP-1999; 99EP-00118630.
 PR 21-SEP-1999; 99EP-00118631.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX
 DR WPI; 2001-335469/35.
 XX
 XX New peptide useful for combating the autoantibodies that are responsible
 PT for dilative cardiomyopathy.
 XX
 PS Claim 4; Page 22; 29pp; German.
 XX
 CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta 1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 14 AA;

Query Match 100.0%; Score 46; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.075;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
 |||||
 Db 2 GSFFSELM 9

RESULT 4
 AAB86020
 ID AAB86020 standard; peptide; 14 AA.
 XX
 AC AAB86020;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM autoantibody-associated peptide #1.
 XX
 KW DCM; dilative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
 KW autoantibody; myocardial.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetylated"
 FT Modified-site 14
 FT /note= "C-terminal amide"
 FT

XX
 PN DE19945211-A1.
 XX
 PD 29-MAR-2001.
 XX

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PF 21-SEP-1999; 99DE-01045211.
XX
PR 21-SEP-1999; 99DE-01045211.
XX
PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX
DR WPI; 2001-301259/32.
XX
XX New autoantibody-binding peptides with an amino acid sequence
PT corresponding to a beta1-adrenergic receptor group useful for treating
PT dilatative cardiomyopathy.
XX
XX Claim 2; Page 5; 8pp; German.
XX
CC This invention describes novel peptides (I) with an amino acid sequence
CC corresponding to a beta1-adrenergic receptor group recognized by
CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
CC invention also describes a chromatographic device comprising (I) bound to
CC a solid phase. The products of the invention have cardiant activity. (I)
CC are useful for treating DCM by binding autoantibodies directed against
CC myocardial beta1-adrenergic receptors, either by neutralizing the
CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
CC (I) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX
XX Sequence 14 AA;
XX
Query Match 100.0%; Score 46; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GSFFSELW 8
DB 2 GSFFSELW 9
XX
RESULT 5
AAB86013
ID AAB86013 standard; peptide; 15 AA.
XX
AC AAB86013;
XX
DT 12-JUL-2001 (first entry)
XX
DE DCM-associated peptide #13.
XX
XX DCM; dilatative cardiomyopathy; autoantibody; cardiant;
KW beta-1 adrenergic activated antibody; immunosuppressive.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 15 /note= "Lys modified with an amide or free acid group"
FT FT
XX
XX WO200121660-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-2000; 2000WO-EP009241.
XX
XX 21-SEP-1999; 99EP-00118630.
XX
XX 21-SEP-1999; 99EP-00118631.
XX
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX
XX WPI; 2001-335469/35.
XX
XX New peptide useful for combating the autoantibodies that are responsible
PT

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PT for dilatative cardiomyopathy.
XX
PS Claim 4; Page 22; 29pp; German.
XX
CC This invention describes a novel peptide (P1) which can be used for (1)
CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
CC of the invention have cardiant and immunosuppressive activity. (P1) is
CC used to produce medicine to combat beta1 adrenergic activated
CC autoantibodies having a causal pathological relationship with dilatative
CC cardiomyopathy. This sequence represents a specifically claimed peptide
CC used to illustrate the method of the invention
XX
XX Sequence 15 AA;
XX
Query Match 100.0%; Score 46; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GSFFSELW 8
DB 3 GSFFSELW 10
XX
RESULT 6
AAB86021
ID AAB86021 standard; peptide; 15 AA.
XX
AC AAB86021;
XX
DT 12-JUL-2001 (first entry)
XX
DE DCM autoantibody-associated peptide #2.
XX
XX DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
KW autoantibody; myocardial.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetylated"
FT FT
FT Modified-site 15 /note= "C-terminal amide"
FT FT
XX
XX DE19945211-A1.
XX
XX 29-MAR-2001.
XX
XX 21-SEP-1999; 99DE-01045211.
XX
XX 21-SEP-1999; 99DE-01045211.
XX
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX
XX WPI; 2001-301259/32.
XX
XX New autoantibody-binding peptides with an amino acid sequence
PT corresponding to a beta1-adrenergic receptor group useful for treating
PT dilatative cardiomyopathy.
XX
XX Claim 2; Page 5; 8pp; German.
XX
XX This invention describes novel peptides (I) with an amino acid sequence
XX corresponding to a beta1-adrenergic receptor group recognized by
XX autoantibodies associated with dilatative cardiomyopathy (DCM). The
XX invention also describes a chromatographic device comprising (I) bound to
XX a solid phase. The products of the invention have cardiant activity. (I)
XX are useful for treating DCM by binding autoantibodies directed against
XX myocardial beta1-adrenergic receptors, either by neutralizing the
XX antibodies in vivo or by extracorporeal treatment of blood or plasma with
XX antibodies in vivo or by extracorporeal treatment of blood or plasma with
XX

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CC (1) Immobilized on a solid phase. This sequence represents a specifically
 CC claimed peptide used to illustrate the method of the invention

SQ Sequence 15 AA;

Query Match 100.0%; Score 46; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFFSELM 8
 |||||
 Db 3 GSFFSELM 10

RESULT 7

AAB86009
 ID AAB86009 standard; peptide; 13 AA.

XX AC AAB86009;

XX DT 12-JUL-2001 (first entry)

XX DE DCM-associated peptide #9.

XX KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.

XX OS Synthetic.

XX XN WO200121660-A1.

XX PD 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-EP009241.

XX PR 21-SEP-1999; 99EP-00118630.

XX PR 21-SEP-1999; 99EP-00118631.

XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX DR WPI; 2001-335469/35.

XX PT New peptide useful for combating the autoantibodies that are responsible
 PT for dilatative cardiomyopathy.

XX PS Claim 3; Page 21; 29pp; German.

XX CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta 1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilatative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention

SQ Sequence 13 AA;

Query Match 65.2%; Score 30; DB 4; Length 13;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELM 8
 ||:|:
 Db 3 GTLFSDFW 10

RESULT 8

AAB86007

ID AAB86007 standard; peptide; 13 AA.

XX

AC AAB86007;

XX DT 12-JUL-2001 (first entry)

XX DE DCM-associated peptide #7.

XX KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.

XX OS Synthetic.

XX XN WO200121660-A1.

XX PD 29-MAR-2001.

XX PF 21-SEP-2000; 2000WO-EP009241.

XX PR 21-SEP-1999; 99EP-00118630.

XX PR 21-SEP-1999; 99EP-00118631.

XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.

XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;

XX DR WPI; 2001-335469/35.

XX PT New peptide useful for combating the autoantibodies that are responsible
 PT for dilatative cardiomyopathy.

XX PS Claim 3; Page 21; 29pp; German.

XX CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta 1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilatative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention

SQ Sequence 13 AA;

Query Match 65.2%; Score 30; DB 4; Length 13;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSFFSELM 8
 ||:|:
 Db 3 GTLFSDFW 10

RESULT 9

AAM47221

ID AAM47221 standard; peptide; 13 AA.

XX AC AAM47221;

XX DT 12-FEB-2002 (first entry)

XX DE Dilated cardiomyopathy absorbents related peptide #1.
 XX KW Dilated cardiomyopathy; absorbent; betal adrenoreceptor;
 KW M2 muscarine receptor; antibody.

XX OS Synthetic.

XX XN WO200176662-A1.

XX PD 18-OCT-2001.

XX PF 09-APR-2001; 2001WO-JP003026.

XX PR 07-APR-2000; 2000JP-00106915.

```

XX PA (KANF ) KANEKA CORP.
XX PI Ogino E, Furiyoshi S, Hirai F, Nishimoto T;
XX DR WPI; 2002-041274/05.
XX Adsobernts for dilated cardiomyopathy, comprises an immobilized compound
PT capable of selectively removing antibodies against approximately b1
PT adrenoceptor and/or M2 muscarine receptors in body fluid without
PT pretreatment.
XX Claim 3; Page 21; 37pp; Japanese.
XX The present invention relates to a method of immobilising an adsorbent
CC with a compound capable of binding to an antibody against betal
CC adrenoceptor and/or an antibody against M2 muscarine receptor on a
CC water-insoluble support. The adsorbents, apparatus and method are useful
CC for treating dilated cardiomyopathy by removing antibodies against betal
CC adrenoceptor and/or M2 muscarine receptor. The present sequence is a
CC peptide described in the exemplification of the invention
XX SQ Sequence 13 AA;
Query Match 65.2%; Score 30; DB 5; Length 13;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GSFFSEL 7
DB |||||
7 GSFFCEL 13
RESULT 10
AAB86028
ID AAB86028 standard; peptide; 15 AA.
XX AC
XX AAB86028;
DT 12-JUL-2001 (first entry)
XX DCM autoantibody-associated peptide #2.
XX DCM; autoantibody; beta-1-adrenergic receptor; dilatative cardiomyopathy;
KW cardiand; myocardial.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site 15 /note= "N-terminal acetylated"
FT Modified-site 15 /note= "C-terminal amide"
XX DE19945210-A1.
XX PN
XX 29-MAR-2001.
XX 21-SEP-1999; 99DE-01045210.
XX 21-SEP-1999; 99DE-01045210.
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX WPI; 2001-301258/32.
XX New autoantibody-binding peptides with an amino acid sequence
PT corresponding a betal-adrenergic receptor group, useful for treating
PT dilatative cardiomyopathy.
XX Claim 2; Page 5; 8pp; German.
XX PS
XX This invention describes novel peptides (I) with an amino acid sequence
CC corresponding a beta-1-adrenergic receptor group recognized by
CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
CC products of the invention have cardiant activity. (I) are useful for
CC treating DCM by binding autoantibodies directed against myocardial beta-1
CC -adrenergic receptors, either by neutralizing the antibodies in vivo or
CC by extracorporeal treatment of blood or plasma with (I) immobilized on a
CC solid phase. This sequence represents a specifically claimed peptide used
CC to illustrate the method of the invention
XX SQ Sequence 15 AA;
Query Match 65.2%; Score 30; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 GSFFSELW 8
DB :|||
3 GTLFSDFW 10
RESULT 11
AAB86017
ID AAB86017 standard; peptide; 15 AA.
XX AC
XX AAB86017;
DT 12-JUL-2001 (first entry)
XX DCM-associated peptide #17.
XX DCM; dilatative cardiomyopathy; autoantibody; cardiant;
KW beta-1 adrenergic activated antibody; immunosuppressive.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 15
FT Modified-site 15 /note= "Lys modified with an amide or free acid group"
FT WO200121660-A1.
XX PN
XX 29-MAR-2001.
XX 21-SEP-2000; 2000WO-BP009241.
XX 21-SEP-1999; 99EP-00118630.
XX 21-SEP-1999; 99EP-00118631.
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX WPI; 2001-335469/35.
XX New peptide useful for combating the autoantibodies that are responsible
PT for dilatative cardiomyopathy.
XX Claim 4; Page 22; 29pp; German.
XX This invention describes a novel peptide (P1) which can be used for (1)
CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
CC of the invention have cardiant and immunosuppressive activity. (P1) is
CC used to produce medicine to combat beta 1 adrenergic activated
CC autoantibodies having a causal pathological relationship with dilatative
CC cardiomyopathy. This sequence represents a specifically claimed peptide
CC used to illustrate the method of the invention
XX SQ Sequence 15 AA;
Query Match 65.2%; Score 30; DB 4; Length 15;

```

Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
|: |: |
Db 3 GTLFSDFW 10

RESULT 12
AAB86014
ID AAB86014 standard; peptide; 15 AA.
XX AC
AC AAB86014;
XX
DT 12-JUL-2001 (first entry)
XX
DE DCM-associated peptide #14.
XX
KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
KW beta-1 adrenergic activated antibody; immunosuppressive.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 15
FT /note= "Lys modified with an amide or free acid group"
XX
PN WO200121660-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-EPO9241.
XX
PR 21-SEP-1999; 99EP-00118630.
PR 21-SEP-1999; 99EP-00118631.
XX
PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX
DR WPI; 2001-335469/35.
XX
PT New peptide useful for combating the autoantibodies that are responsible
PT for dilatative cardiomyopathy.
XX
PS Claim 4; Page 22; 29pp; German.
XX
SQ This invention describes a novel peptide (P1) which can be used for (1)
CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
CC of the invention have cardiant and immunosuppressive activity. (P1) is
CC used to produce medicine to combat beta-1 adrenergic activated
CC autoantibodies having a causal pathological relationship with dilatative
CC cardiomyopathy. This sequence represents a specifically claimed peptide
CC used to illustrate the method of the invention
XX

Query Match 65.2%; Score 30; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
|: |: |
Db 3 GTLFSDFW 10

RESULT 13
AAB86022
ID AAB86022 standard; peptide; 15 AA.
XX AC
AC AAB86022;
XX

Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
|: |: |
Db 3 GTLFSDFW 10

RESULT 14
AAO20307
ID AAO20307 standard; peptide; 15 AA.
XX
AC AAO20307;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human plectin 10 protein N-terminal region.
XX
KW Human; plectin 10; DNA recombination; cancer; HIV infection.
XX
OS Homo sapiens.
XX
PN CN1325901-A.
XX

DT 12-JUL-2001 (first entry)
XX
DE DCM autoantibody-associated peptide #3.
XX
KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
KW autoantibody; myocardial.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetylated"
FT Modified-site 15
FT /note= "C-terminal amide"
XX
PN DE19945211-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-1999; 99DE-01045211.
XX
PR 21-SEP-1999; 99DE-01045211.
XX
PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX
DR WPI; 2001-301259/32.
XX
PT New autoantibody-binding peptides with an amino acid sequence
PT corresponding a beta-1-adrenergic receptor group useful for treating
PT dilatative cardiomyopathy.
XX
PS Claim 2; Page 5; 8pp; German.
XX
SQ This invention describes novel peptides (I) with an amino acid sequence
CC corresponding a beta-1-adrenergic receptor group recognized by
CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
CC invention also describes a chromatographic device comprising (I) bound to
CC a solid phase. The products of the invention have cardiant activity. (I)
CC are useful for treating DCM by binding autoantibodies directed against
CC myocardial beta-1-adrenergic receptors, either by neutralizing the
CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
CC (I) immobilized on a solid phase. This sequence represents a specifically
CC claimed peptide used to illustrate the method of the invention
XX

Query Match 65.2%; Score 30; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
|: |: |
Db 3 GTLFSDFW 10

RESULT 14
AAO20307
ID AAO20307 standard; peptide; 15 AA.
XX
AC AAO20307;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human plectin 10 protein N-terminal region.
XX
KW Human; plectin 10; DNA recombination; cancer; HIV infection.
XX
OS Homo sapiens.
XX
PN CN1325901-A.
XX

```

PD 12-DEC-2001.
XX
PF 31-MAY-2000; 2000CN-00116269.
XX
PR 31-MAY-2000; 2000CN-00116269.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-196661/26.
XX
PT Polypeptide-human plectin 10 and polynucleotide encoding it.
XX
PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The invention relates to the novel polypeptide-human plectin 10, the
CC polynucleotide encoding it, the process for preparing the polypeptide by
CC DNA recombination, the application of the polypeptide in treating
CC diseases such as cancer and HIV infection. The invention also relates to
CC the antagonist of the polypeptide and its medical action, and the
CC application of the polynucleotide. This sequence represents an N-terminal
CC region of the human plectin 10 protein of the invention
XX
SQ Sequence 15 AA;
    Query Match      65.2%; Score 30; DB 5; Length 15;
    Best Local Similarity 57.1%; Pred. No. 81;
    Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPFSESLW 8
Db :|||:|

RESULT 15
ABJ37231
ID ABJ37231 standard; peptide; 15 AA.
XX
AC ABJ37231;
XX
DT 08-MAY-2003 (first entry)
XX
DE Rhodopsin related G-protein coupled receptor binding site peptide #107.
XX
KW Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
XX Rhodopsin.
XX
OS Unidentified.
XX
PN WC2003004147-A2.
XX
PD 16-JAN-2003.
XX
PF 05-JUL-2002; 2002WO-GB003094.
XX
PR 06-JUL-2001; 2001GB-00016570.
XX
PA (BIOF-) BIOFOCUS PLC.
XX
PI Crossley R, Rose VS, Stevens AP;
XX
DR WPI; 2003-221549/21.
XX
PT Producing compound library, by generating biological target model using
PT target sequence information, defining microenvironments interacting with
PT ligand and motifs interacting with microenvironment, and assembling
PT motifs.
XX
PS Disclosure; Fig 1; 39pp; English.
XX
CC The invention relates to a novel method for producing a compound library.
CC The novel method involves reducing a biological target into a group of

```

```

CC one or more amino acids required for interaction with a ligand, to
CC generate a model of the biological target, using the model to define a
CC microenvironment in the biological target capable of interacting with the
CC ligand, defining motifs which interact with the microenvironment, and
CC assembling the motifs to generate a compound library for screening. The
CC novel method is useful to produce compound libraries for screening
CC natural ligands such as peptides and proteins or for producing chemical
CC compounds based on drug motifs for screening. This sequence represents a
CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,
CC which relates to the novel compound library production method of the
CC invention
XX
SQ Sequence 15 AA;
    Query Match      63.0%; Score 29; DB 6; Length 15;
    Best Local Similarity 62.5%; Pred. No. 1.3e+02;
    Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFSESLW 8
Db :|||:|
    1 GSFVSPFW 8

Search completed: September 20, 2004, 17:30:54
Job time : 54 secs

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Blank

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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:31:56 ; Search time 124 Seconds
(without alignments)
20.718 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gssffselw 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 58621

Minimum DB seq length: 11

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
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5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	65.2	13	16	US-10-221-042-1
2	28	60.9	14	10	US-09-964-821B-53
3	28	60.9	14	14	US-10-268-332-53
4	27	58.7	11	10	US-09-840-085-31
5	27	58.7	12	9	US-09-214-371-17
6	27	58.7	12	9	US-09-214-371-24
7	27	58.7	12	9	US-09-214-371-25
8	27	58.7	12	12	US-10-609-217-131
9	27	58.7	12	12	US-10-609-217-132
10	27	58.7	12	12	US-10-609-217-133
11	27	58.7	12	12	US-10-609-217-143
12	27	58.7	12	12	US-10-632-388-131
13	27	58.7	12	12	US-10-632-388-132
14	27	58.7	12	12	US-10-632-388-143
15	27	58.7	12	12	US-10-632-388-144

16	27	58.7	12	12	US-10-651-723-131	Sequence 131, App
17	27	58.7	12	12	US-10-651-723-132	Sequence 132, App
18	27	58.7	12	12	US-10-651-723-143	Sequence 143, App
19	27	58.7	12	12	US-10-651-723-144	Sequence 144, App
20	27	58.7	12	12	US-10-645-761-131	Sequence 131, App
21	27	58.7	12	12	US-10-645-761-132	Sequence 132, App
22	27	58.7	12	12	US-10-645-761-143	Sequence 143, App
23	27	58.7	12	12	US-10-645-761-144	Sequence 144, App
24	27	58.7	12	16	US-10-666-696-131	Sequence 131, App
25	27	58.7	12	16	US-10-666-696-132	Sequence 132, App
26	27	58.7	12	16	US-10-666-696-143	Sequence 143, App
27	27	58.7	12	16	US-10-666-696-144	Sequence 144, App
28	27	58.7	12	16	US-10-653-048-131	Sequence 131, App
29	27	58.7	12	16	US-10-653-048-132	Sequence 132, App
30	27	58.7	12	16	US-10-653-048-143	Sequence 143, App
31	27	58.7	12	16	US-10-653-048-144	Sequence 144, App
32	27	58.7	14	12	US-10-275-427A-13	Sequence 13, Appl
33	27	58.7	15	9	US-09-732-384-6	Sequence 6, Appl
34	27	58.7	15	12	US-10-425-970-4	Sequence 4, Appl
35	27	58.7	15	14	US-10-211-088-141	Sequence 141, App
36	26	56.5	14	12	US-10-393-815-253	Sequence 253, App
37	25	54.3	11	9	US-09-881-276-6	Sequence 6, Appl
38	25	54.3	11	14	US-10-097-175-60	Sequence 60, Appl
39	25	54.3	15	14	US-10-005-530-28	Sequence 28, Appl
40	24.5	53.3	14	10	US-09-962-756-1930	Sequence 1930, Ap
41	24.5	53.3	14	15	US-10-253-471-1930	Sequence 1930, Ap
42	24.5	53.3	14	16	US-10-253-493-1930	Sequence 1930, Ap
43	24	52.2	12	14	US-10-032-818-31	Sequence 31, Appl
44	24	52.2	12	14	US-10-286-457-256	Sequence 256, App
45	24	52.2	12	15	US-10-394-511-69	Sequence 69, Appl

ALIGNMENTS

RESULT 1

US-10-221-042-1
; Sequence 1, Application US/10221042
; Publication No. US20040120946A1
; GENERAL INFORMATION:
; APPLICANT: KANEKA CORPORATION
; TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY
; FILE REFERENCE: 12218/5
; CURRENT APPLICATION NUMBER: US/10/221,042
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: PCT/JP01/03026
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: JP 2000-106915
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Peptide having a binding affinity for an antibody against
; OTHER INFORMATION: beta1-adrenoceptor and/or an antibody against M2 muscarinic recep
; OTHER INFORMATION: tor
US-10-221-042-1

Query Match 65.2%; Score 30; DB 16; Length 13;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSSFFSEL 7

Db 7 GSSFFCEL 13

RESULT 2
US-09-964-821B-53
; Sequence 53, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CRACCE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M. G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY3.
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042NP
; CURRENT APPLICATION NUMBER: US/09/964,821B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,783
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,171
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: polypeptide
US-09-964-821B-53

Query Match 60.9%; Score 28; DB 10; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSELMW 8
|||
Db 6 SFSDELW 12

RESULT 3
US-10-268-332-53
; Sequence 53, Application US/10268332
; Publication No. US20030175748A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRMY3, EXPRESSED HIGHLY
; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-53

Query Match 60.9%; Score 28; DB 10; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSELMW 8
|||
Db 6 SFSDELW 12

Query Match 60.9%; Score 28; DB 14; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSELMW 8
|||
Db 6 SFSDELW 12

RESULT 4
US-09-840-085-31
; Sequence 31, Application US/09840085
; Publication No. US20030166240A1
; GENERAL INFORMATION:
; APPLICANT: Schepartz Shrader, Alanna
; APPLICANT: Chin, Jason W. K.
; APPLICANT: Zutshi, Reena
; APPLICANT: Rutledge, Stacey E.
; APPLICANT: Kehlbeck Martin, Joanne D.
; APPLICANT: Zondlo, Neal J.
; TITLE OF INVENTION: DNA and Protein Binding Miniature Proteins
; FILE REFERENCE: 44574-5099-US
; CURRENT APPLICATION NUMBER: US/09/840,085
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,408
; PRIOR FILING DATE: 2000-04-24
; PRIOR APPLICATION NUMBER: US 60/240,566
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US PROVISIONAL
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US PROVISIONAL
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: p53 miniature
; OTHER INFORMATION: protein p53AD
US-09-840-085-31

Query Match 58.7%; Score 27; DB 10; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELMW 8
|||
Db 3 FSDLMW 7

RESULT 5
US-05-214-371-17
; Sequence 17, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Botter, Volker
; APPLICANT: Botter, Angelica
; APPLICANT: Pickles, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83

Query Match 58.7%; Score 27; DB 10; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELMW 8
|||
Db 3 FSDLMW 7

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-17
```

```
Query Match          58.7%; Score 27; DB 9; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 FSELW 8
        ||:||
Db      4 FSDLW 8
```

RESULT 6

```
US-09-214-371-24
; Sequence 24, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
```

```
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Gln
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
```

```
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-09-214-371-24
```

```
Query Match          58.7%; Score 27; DB 9; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 FSELW 8
        ||:||
Db      4 FSDLW 8
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RESULT 7

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US-09-214-371-25
; Sequence 25, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
```

```
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Ac-Gln
; NAME/KEY: VARIANT
; LOCATION: (12)
; OTHER INFORMATION: X = Pro-NH2
```

```
US-09-214-371-25
```

```
Query Match          58.7%; Score 27; DB 9; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 FSELW 8
        ||:||
Db      4 FSDLW 8
```

RESULT 8

```
US-10-609-217-131
; Sequence 131, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-131
```

```
Query Match          58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 FSELW 8
        ||:||
Db      4 FSDLW 8
```

RESULT 9

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US-10-609-217-132
; Sequence 132, Application US/10609217
; Publication No. US20040044188A1
```

; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-132

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 10
US-10-609-217-143
; Sequence 143, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 143
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-143

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 11
US-10-609-217-144
; Sequence 144, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH

; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 144
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-609-217-144

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 12
US-10-632-388-131
; Sequence 131, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 131
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-131

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 13
US-10-632-388-132
; Sequence 132, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-132

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 14
US-10-632-388-143
; Sequence 143, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-143

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

RESULT 15
US-10-632-388-144
; Sequence 144, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA

; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
US-10-632-388-144

Query Match 58.7%; Score 27; DB 12; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
||:|
Db 4 FSDLW 8

Search completed: September 20, 2004, 17:42:42
Job time : 125 secs

99/62K

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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:30:00 ; Search time 17 Seconds
(without alignments)
24.295 Million cell updates/sec

Title: AUDET-SEQ1
Perfect score: 46
Sequence: 1 gsfsselw 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 42678

Minimum DB seq length: 11
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	65.2	11	1	US-08-424-957-42
2	30	65.2	11	3	US-09-035-686-42
3	27	58.7	11	1	US-08-277-660A-9
4	27	58.7	11	1	US-08-277-660A-10
5	27	58.7	11	1	US-08-277-660A-11
6	27	58.7	11	1	US-08-277-660A-12
7	27	58.7	11	1	US-08-277-660A-13
8	27	58.7	11	1	US-08-277-660A-19
9	27	58.7	11	1	US-08-277-660A-20
10	27	58.7	11	1	US-08-424-957-17
11	27	58.7	11	1	US-08-424-957-23
12	27	58.7	11	1	US-08-424-957-24
13	27	58.7	11	1	US-08-424-957-25
14	27	58.7	11	1	US-08-424-957-26
15	27	58.7	11	1	US-08-424-957-32
16	27	58.7	11	1	US-08-424-957-33
17	27	58.7	11	1	US-08-424-957-34
18	27	58.7	11	1	US-08-424-957-36
19	27	58.7	11	1	US-08-424-957-43
20	27	58.7	11	3	US-09-035-686-17
21	27	58.7	11	3	US-09-035-686-23
22	27	58.7	11	3	US-09-035-686-24
23	27	58.7	11	3	US-09-035-686-25
24	27	58.7	11	3	US-09-035-686-26
25	27	58.7	11	3	US-09-035-686-32
26	27	58.7	11	3	US-09-035-686-33
27	27	58.7	11	3	US-09-035-686-34

Sequence 36, Appl
Sequence 43, Appl
Sequence 5, Appl
Sequence 131, Appl
Sequence 132, Appl
Sequence 143, Appl
Sequence 144, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 45, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 44, Appl
Sequence 45, Appl

28 27 58.7 11 3 US-09-035-686-36
29 27 58.7 11 3 US-09-035-686-43
30 27 58.7 11 4 US-09-603-082-5
31 27 58.7 12 4 US-09-428-082B-131
32 27 58.7 12 4 US-09-428-082B-132
33 27 58.7 12 4 US-09-428-082B-143
34 27 58.7 12 4 US-09-428-082B-144
35 27 58.7 15 1 US-08-277-660A-1
36 27 58.7 15 1 US-08-277-660A-4
37 27 58.7 15 1 US-08-424-957-1
38 27 58.7 15 1 US-08-424-957-20
39 27 58.7 15 3 US-09-035-686-1
40 27 58.7 15 3 US-09-035-686-20
41 25 54.3 11 1 US-08-424-957-44
42 25 54.3 11 1 US-08-424-957-45
43 25 54.3 11 1 US-08-424-957-46
44 25 54.3 11 3 US-09-035-686-44
45 25 54.3 11 3 US-09-035-686-45

ALIGNMENTS

RESULT 1
US-08-424-957-42
; Sequence 42, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Pickaley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and p53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-42

Query Match 65.2%; Score 30; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8

Db |||||
 5 FSELM 9

RESULT 2

US-09-035-686-42
; Sequence 42, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-42

Query Match 65.2%; Score 30; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELM 8
 |||||
Db 5 FSELM 9

RESULT 3

US-08-277-660A-9
; Sequence 9, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-277-660A-9

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELM 8
 |||||
Db 5 FSELM 9

RESULT 4

US-08-277-660A-10
; Sequence 10, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:


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;
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-13

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
Db 5 FSDLW 9

RESULT 8
US-08-277-660A-19
; Sequence 19, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,660A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-60244/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-277-660A-20

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
Db 5 FSDLW 9

RESULT 10
US-08-277-660A-19
; Sequence 19, Application US/08277660A
; Patent No. 5702908
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/424,957
;; FILING DATE: 19-APR-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/277,660
;; FILING DATE: 20-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Walter H.
;; REGISTRATION NUMBER: 24,190
;; REFERENCE/DOCKET NUMBER: A-61228/WHd
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-08-424-957-17

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
Db 5 FSDLW 9

RESULT 11
US-08-424-957-23
; Sequence 23, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-08-424-957-23

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
Db 5 FSDLW 9

RESULT 12
US-08-424-957-24
; Sequence 24, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-24

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
Db 5 FSDLW 9

RESULT 13
US-08-424-957-25
; Sequence 25, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:

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;
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-25

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
Db 5 FSDLW 9

RESULT 14
US-08-424-957-26
; Sequence 26, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-26
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; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-26

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
Db 5 FSDLW 9

RESULT 15
US-08-424-957-32
; Sequence 32, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHd
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; US-08-424-957-32
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US-08-424-957-32

Query Match 58.7%; Score 27; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
||:|
Db 5 FSDLW 9

Search completed: September 20, 2004, 17:32:33
Job time : 18 secs

Blink

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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:28:40 ; Search time 36 Seconds
(without alignments)
70.115 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gffselw 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2511

Minimum DB seq length: 11

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	52.2	11	7	O77896 oreochromis
2	23	50.0	11	2	P83537 lactobacill
3	23	50.0	11	7	O77895 oreochromis
4	23	50.0	13	8	Q9XLI2 bemisia tab
5	23	50.0	15	2	Q9R5D6 chromatium
6	22	47.8	12	6	Q9TRT7 bos taurus
7	20	43.5	11	7	O77898 oreochromis
8	20	43.5	11	7	O77894 oreochromis
9	20	43.5	12	6	O46664 macropus ro
10	19	41.3	11	4	Q9UC46 homo sapien
11	19	41.3	12	2	Q53579 rhodobacter
12	19	41.3	13	5	Q812E2 plasmodium
13	19	41.3	15	2	O47892 fremyella d
14	19	41.3	15	2	Q53580 rhodobacter
15	19	41.3	15	2	Q47893 fremyella d
16	19	41.3	15	11	Q923G8 rattus norv

17	18	39.1	12	13	Q8UVW0
18	18	39.1	14	13	Q8J80
19	18	39.1	15	2	Q8R4K0
20	18	39.1	15	8	Q8HIF8
21	18	39.1	15	8	Q8HIF6
22	17.5	38.0	11	8	Q9G5Z2
23	17.5	38.0	15	5	Q9TWD5
24	17	37.0	11	13	Q9PS64
25	17	37.0	13	2	Q55234
26	17	37.0	14	2	Q9R518
27	17	37.0	14	6	O77538
28	17	37.0	15	5	Q17067
29	17	37.0	15	5	P81831
30	17	37.0	15	11	Q35411
31	17	37.0	15	13	Q9PS61
32	16	34.8	11	13	Q7ZZ19
33	16	34.8	11	13	Q7ZZ16
34	16	34.8	12	4	Q9BY9
35	16	34.8	12	5	Q9TY9
36	16	34.8	12	6	Q9BFT6
37	16	34.8	12	6	Q9BFV6
38	16	34.8	12	6	Q9BFR6
39	16	34.8	12	6	Q9BFS3
40	16	34.8	12	6	Q9BFV1
41	16	34.8	12	6	Q9BFT7
42	16	34.8	12	6	Q9BFR4
43	16	34.8	12	6	Q9BFT9
44	16	34.8	12	6	Q9BFS9
45	16	34.8	12	6	Q9BFR3

ALIGNMENTS

RESULT 1

O77896 PRELIMINARY; PRT; 11 AA.
AC O77896
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.,
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci."
RL Genetics 149:1527-1537(1998).
DR TMEL; AF050006; AAC41345.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match 52.2%; Score 24; DB 7; Length 11;
Best Local Similarity 56.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFESEW 8
Db 3 FWSMLW 8

RESULT 2

P83537 PRELIMINARY; PRT; 11 AA.
ID P83537

AC P83537;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 Lactobacillus sanfranciscensis";
 RL Proteomics 2:765-774 (2002).
 CC -I- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
 CC PROTEIN IS: 65 KDA.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 50.0%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSPFS 5
 |||||
 Db 1 GSPFA 5

RESULT 3
 Q77895
 ID Q77895 PRELIMINARY; PRT; 11 AA.
 AC Q77895;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1537 (1998).
 DR EMBL; AF050005; AAC41344.1; -.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;

Query Match 50.0%; Score 23; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 7.1e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFSILW 8
 |||||
 Db 3 FWSILW 8

RESULT 4
 Q9XLI2
 ID Q9XLI2 PRELIMINARY; PRT; 13 AA.
 AC Q9XLI2;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 OS Bemisia tabaci (Sweetpotato whitefly).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
 OC Aleyrodidae; Aleyrodinae; Aleyrodinae; Bemisia.
 OX NCBI_TaxID=7038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10583831;
 RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
 RA Brown J.K.;
 RT "A phylogeographical analysis of the Bemisia tabaci species complex
 based on mitochondrial DNA markers";
 RL Mol. Ecol. 8:1683-1691 (1999).
 DR EMBL; AF110703; AAD28415.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 50.0%; Score 23; DB 8; Length 13;
 Best Local Similarity 42.9%; Pred. No. 8.4e+02;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSELW 8
 |||||
 Db 1 SYFTSSW 7

RESULT 5
 Q9RSD6
 ID Q9RSD6 PRELIMINARY; PRT; 15 AA.
 AC Q9RSD6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein
 DE (Fragment).
 OS Chromatium vinosum.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 OC Chromataceae; Allochromatium.
 OX NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93146381; PubMed=1490603;
 RA Liebergessel M., Schmidt B., Steinbuechel A.;
 RT "Isolation and identification of granule-associated proteins relevant
 for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
 D.";
 RL FEMS Microbiol. Lett. 78:227-232 (1992).
 SQ SEQUENCE 15 AA; 1874 MW; 165FA9A16BCA2A9D CRC64;

Query Match 50.0%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 9.7e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SFFSELW 8
 |||||
 Db 5 NFENDDW 11

RESULT 6
 Q9TRT7
 ID Q9TRT7 PRELIMINARY; PRT; 12 AA.
 AC Q9TRT7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 15 kDa amyloid protein A homolog (Fragment).

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92132498; PubMed=1734497;
RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
of bovine kidney.";
RL Scand. J. Immunol. 35:63-69(1992).
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;

Query Match 47.8%; Score 22; DB 6; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SPFSELM 8
Db 1 SPFXEY 7

RESULT 7
O77898 PRELIMINARY; PRT; 11 AA.
AC O77898
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050008; AAC41347.1; -.
FT NON_TER 1
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 43.5%; Score 20; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFSELM 8
Db 3 FWSIVM 8

RESULT 8
O77894 PRELIMINARY; PRT; 11 AA.
AC O77894
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;

OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050004; AAC41343.1; -.
FT NON_TER 1
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 43.5%; Score 20; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFSELM 8
Db 3 FWSIVM 8

RESULT 9
O46664 PRELIMINARY; PRT; 12 AA.
AC O46664
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
GN G6PD.
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53774; AAC48789.1; -.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;

Query Match 43.5%; Score 20; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSPFSE 6
Db 2 GGXFDE 7

RESULT 10
Q9UC46 PRELIMINARY; PRT; 11 AA.
AC Q9UC46
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neutrophil inhibitor peptide, NIP=POLYMORPHONUCLEAR neutrophil
inhibitor peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=96326114; PubMed=8703476;
RA Cooper J.A.Jr., Culbreth R.R.;
RT "Characterization of a neutrophil inhibitor peptide harvested from
RT human bronchial lavage: homology to influenza A nucleoprotein.";
RL Am. J. Respir. Cell Mol. Biol. 15:207-215(1996).
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0030236; P:anti-inflammatory response; NAS.
SQ SEQUENCE 11 AA; 1262 MW; 951A1C3279C9DB45 CRC64;

Query Match 41.3%; Score 19; DB 4; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFF 4
Db 3 GSYP 6

RESULT 11
ID Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa
RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR ENBL; S97551; AAC60405.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6EA8A70532B CRC64;

Query Match 41.3%; Score 19; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSELW 8
Db 2 SKPYKIW 8

RESULT 12
ID Q812E2 PRELIMINARY; PRT; 13 AA.
AC Q812E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
GN PPA0655W.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255709; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mangall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

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RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR ENBL; AL031744; CAD48947.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match 41.3%; Score 19; DB 5; Length 13;
Best Local Similarity 60.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SFFSE 6
Db 7 TFYSE 11

RESULT 13
ID Q47892 PRELIMINARY; PRT; 15 AA.
AC Q47892;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta-allophycocyanin (Fragment).
OS Fremyella diplosiphon (Fragment).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=1086870;
RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
RT the genome of the cyanobacterium Fremyella diplosiphon.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3924-3928(1986).
DR ENBL; M13216; AAA24871.1; -.
FT NON TER 1
SQ SEQUENCE 15 AA; 1644 MW; 9727165699F462F CRC64;

Query Match 41.3%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSFF 4
Db 4 GSYP 7

RESULT 14
ID Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa

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Tue Sep 21 08:51:51 2004

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RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97552; AAC60406.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match
Best Local Similarity 41.3%; Score 19; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPFESELM 8
DB 2 SXFYKIW 8

RESULT 15
Q47893 PRELIMINARY; PRT; 15 AA.
AC Q47893;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Beta-phycocyanin (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaeaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86233345; PubMed=3086870;
RA Conley P.B., Lemaux P.G., Lomax T.L., Grossman A.R.;
RT "Genes encoding major light-harvesting polypeptides are clustered on
RL the genome of the cyanobacterium Fremyella diplosiphon.";
DR EMBL; M13217; AAA24880.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1528 MW; 7FF2F65518F493D4 CRC64;

Query Match
Best Local Similarity 41.3%; Score 19; DB 2; Length 15;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFF 4
DB 4 GSYF 7

Search completed: September 20, 2004, 17:31:51
Job time : 38 secs

```

B/ark

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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:28:15 ; Search time 9 Seconds
(without alignments)
46.285 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gsfafslw 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 430

Minimum DB seq length: 11

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	43.5	13	1 NP3_LYMST	P80180 lylnaeaa sta
2	19	41.3	15	1 ALB2_TRASC	P81189 trachemys s
3	18	39.1	11	1 LPW_THETH	P05624 thermus the
4	18	39.1	11	1 TKNA_SCYCA	P41333 scyllorhinu
5	18	39.1	15	1 FIBA_SYNCA	P14463 syncerus ca
6	17	37.0	11	1 MBBI_KLRPN	P80580 klebsiella
7	16	34.8	12	1 FAR7_PENMO	P83322 penaeus mon
8	16	34.8	12	1 UP01_CAEEL	P55954 caenorhabdi
9	16	34.8	14	1 CXAL_CONCN	P56973 conus conso
10	16	34.8	14	1 FIBA_HORSE	P14452 equus cabal
11	16	34.8	15	1 HS11_PINPS	P81083 pinus pinas
12	15	32.6	11	1 CA42_LITCI	P82092 litoria cit
13	15	32.6	13	1 CXA2_CONGE	P01520 conus geogr
14	15	32.6	14	1 KARA_BROPL	P22442 bromelia pl
15	14	30.4	11	1 CORZ_PERAM	P11496 periplaneta
16	14	30.4	12	1 HEP1_BACSE	P83054 bacteroides
17	14	30.4	13	1 CRTC_BOVIN	P28489 bos taurus
18	14	30.4	13	1 NP1_LYMST	P80178 lylnaeaa sta
19	14	30.4	13	1 NP2_LYMST	P80179 lylnaeaa sta
20	14	30.4	13	1 NP4_LYMST	P80181 lylnaeaa sta
21	14	30.4	13	1 NP5_LYMST	P80182 lylnaeaa sta
22	14	30.4	13	1 TEJA_RANJA	P83307 rana japoni
23	14	30.4	14	1 UC34_MAIZE	P80640 zea mays (m
24	14	30.4	15	1 ARCA_STRP5	P58827 streptococc
25	14	30.4	15	1 FK97_PINPS	P81104 pinus pinas
26	14	30.4	15	1 RM01_RAT	P81563 rattus norv
27	14	30.4	15	1 RBS BHYPA	P80657 physcomitre
28	14	30.4	15	1 UC16_MAIZE	P80622 zea mays (m
29	13	28.3	11	1 NUHM_CANPA	P49820 canis famli
30	13	28.3	12	1 UR2_FOLSP	P81022 polyodon sp
31	13	28.3	13	1 ADFE_TENMO	P83109 tenebrio mo
32	13	28.3	13	1 ORCK_ORCLI	P37086 orconectes
33	13	28.3	13	1 UN02_PINPS	P81667 pinus pinas

34 13 28.3 13 1 YPNP_PHOLU P41122 photorhabdu
35 13 28.3 14 1 LPE2_ECOLI P06985 escherichia
36 13 28.3 14 1 LPW_RHIME P18954 rhizobium m
37 13 28.3 14 1 PPK6_PERAM P82693 periplaneta
38 13 28.3 14 1 SMS1_MYOSC P20750 myoxocephal
39 13 28.3 14 1 SMS_ALLMI P31885 alligator m
40 13 28.3 14 1 UN46_CLOPA P81362 clostridium
41 13 28.3 15 1 LPF_ECOLI P03057 escherichia
42 13 28.3 15 1 RMI2_YEAST P36522 saccharomyc
43 13 28.3 15 1 UC14_MAIZE P80620 zea mays (m
44 13 28.3 15 1 UC28_MAIZE P80634 zea mays (m
45 12.5 27.2 12 1 UR2_SCYCA P35490 scyllorhinu

ALIGNMENTS

RESULT 1

NP3_LYMST STANDARD; PRT; 13 AA.

AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lylnae-DP-amide 3.
OS Lylnae stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lylnaeoidea; Lylnaeidae; Lylnaeae.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "LylnaeFamides, a new family of neuropeptides from the pond snail,
RT Lylnae stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?";
RL Eur. J. Biochem. 213:875-879 (1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR; S32473; S32473.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
FT UNSURE 12 12
SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 43.5%; Score 20; DB 1; Length 13;

Best Local Similarity 66.7%; Pred. No. 5.3e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSPFSE 6

DB 7 GSAFSD 12

ALB2_TRASC STANDARD; PRT; 15 AA.

AC P81189;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 68 kDa serum albumin (Alb-2) (Fragment).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;
OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
OX NCBI_TaxID=34903;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103404; PubMed=9440230;
RA Brown M.A., Chambers G.K., Licht P.;
RT "Purification and partial amino acid sequences of two distinct
RT albumins from turtle plasma.";
RL Comp. Biochem. Physiol. 118B:367-374 (1997).

```

CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- MISCELLANEOUS: In the red-eared slider turtle, there are two forms
CC of albumin, ALB-1 and ALB-2.
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
CC InterPro: IPR000264; Serum albumin.
DR PROSITE; PS00212; ALBUMIN; PARTIAL.
KW Metal-binding; Lipid-binding.
FT NON TER 15
SQ SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;

Query Match 41.3%; Score 19; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSPFSEL 7
DB 9 GHXPXEL 15

RESULT 3
LPW THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1998 (Rel. 09, Created)
DT 01-NOV-1998 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Tri operon leader peptide.
GN TREL
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG."
RL Blochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: X07744; CAA30565.1; -.
DR Tryptophan biosynthesis; Leader peptide.
KW Tryptophan
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 39.1%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELW 8
DB 5 SALW 8

RESULT 4
TKNA SCYCA STANDARD; PRT; 11 AA.
ID TKNA_SCYCA
AC P41333;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro: IPR02040; Tachy Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
FT SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D967 CRC64;

Query Match 39.1%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSPF 4
DB 5 GQFF 8

RESULT 5
FIBA SYNCA STANDARD; PRT; 15 AA.
ID FIBA SYNCA
AC P14463;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Syncerus caffer (Cape buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;
OC Bovidae; Bovinae; Syncerus.
OX NCBI_TaxID=9970;
RN [1]
RP SEQUENCE.
RX MEDLINE=67209145; PubMed=6033721;
RA Doolittle R.F., Schubert D., Schwartz S.A.;
RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT Dromedary camel, mule deer, and cape buffalo.";
RL Arch. Biochem. Biophys. 118:456-467(1967).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 15 FIBRINOPEPTIDE A.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;

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Query Match      39.1%; Score 18; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSE 6
   | | | | |
Db 5 GFLAE 10

RESULT 6
MHBI_KLEPN
ID MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE.
RX MEDLINE=96349117; PubMed=8760924;
RA Robson N.D., Parrott S., Cooper R.A.;
RT "In vitro formation of a catabolic plasmid carrying Klebsiella
RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
RT hydroxybenzoate."
RL Microbiology 142:2115-2120(1996).
KW -|- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
FT NON TER 11
FT SEQUENCE 11 AA; 1387 MW; 1E50E2DD49C9D5AB CRC64;

Query Match      37.0%; Score 17; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SFES 5
   | | | |
Db 5 SFEN 8

RESULT 7
FAR7_PENMO
ID FAR7_PENMO STANDARD; PRT; 12 AA.
AC P83322;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYRKPFGNSIF-amide).
OS Peneaus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkaseem C., Longyant S.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon."
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.

FT 40D RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1383 MW; 31209192EF49D777 CRC64;

Query Match      34.8%; Score 16; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFF 4
   | | |
Db 9 GSIF 12

RESULT 8
UP01_CAEEL
ID UP01_CAEEL STANDARD; PRT; 12 AA.
AC P55954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unknown protein from 2D-page (Spot 1) (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE.
RX STRAIN=Bristol N2;
RC MEDLINE=97295999; PubMed=9150941;
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
RT homogenates and identification of protein spots by microsequencing."
RL Electrophoresis 18:557-562(1997).
DR Siena-2DPAGE; P55954; -.
FT NON TER 12
FT SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match      34.8%; Score 16; DB 1; Length 12;
Best Local Similarity 37.5%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GSFFSELM 8
   | | | | |
Db 3 GDDIMEKW 10

RESULT 9
CXAL_CONCN
ID CXAL_CONCN STANDARD; PRT; 14 AA.
AC P56973;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin Cn1A [Contains: Alpha-conotoxin Cn1B].
OS Conus consors (Singed cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101297;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=99255390; PubMed=10320362;
RA Favreau P., Kramm I., le Gall F., Sobenrieth M.J., Lamthanh H.,
RA Bouet F., Servent D., Molgo J., Menez A., Letourneux Y.,
RA Lancelin J.-M.;
RT "Biochemical characterization and nuclear magnetic resonance
RT structure of novel alpha-conotoxins isolated from the venom of Conus
RT consors."
RL Biochemistry 38:6317-6326(1999).
CC -|- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide seems to be a potent and selective
CC blocker of muscular subtype of nAChR.

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CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -I- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; A58963;
DR PDB; 1B45; 09-JUL-99.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
FT Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT PEPTIDE 1 14 ALPHA-CONOTOXIN CNIA.
FT PEPTIDE 3 14 ALPHA-CONOTOXIN CNIB.
FT DISULFID 3 8
FT DISULFID 4 14
FT MOD RES 14 14 AMIDATION.
FT HELIX 6 8
FT TURN 9 10
SQ SEQUENCE 14 AA; 1548 MW; DEE91969BF5ESBD CRC64;

Query Match 34.8%; Score 16; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSPFS 5
DB 9 GKYS 13

RESULT 10
FIBA HORSE
ID FIBA HORSE STANDARD; PRT; 14 AA.
AC P14452;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965);
CC -I- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -I- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -I- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC Blood coagulation; Plasma.
KW PEPTIDE 1 14 FIBRINOPEPTIDE A.
FT PEPTIDE 1 14
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;

Query Match 34.8%; Score 16; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSPFSE 6
DB 4 GEFLHE 9

RESULT 11
HS11 PINPS
ID HS11 PINPS STANDARD; PRT; 15 AA.
AC P81083;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable class I heat shock protein (Water stress responsive protein
DE 3) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RC Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RA "Water-deficit-responsive proteins in maritime pine.";
RT Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RA TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RC Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
RN [3]
RP REVISION TO 1.
RA Frigerio J.-M.;
RL Submitted (SEP-2001) to Swiss-Prot.
CC -I- SUBUNIT: Forms oligomeric structures (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- INDUCTION: By water stress.
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N144) is: 6.1, its MW is: 17 kDa.
CC -I- SIMILARITY: Belongs to the small heat shock protein (HSP20)
CC family.
CC -I- SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II
CC WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST
CC AND CLASS IV WHICH IS IN THE ENOMEMBRANE. THIS PROTEIN BELONGS
CC TO CLASS I.
DR InterPro; IPR002068; Hsp20.
DR PROSITE; PS10131; HSP20; PARTIAL.
KW Heat shock; Multigene family.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1847 MW; 87FC504C2EB1F2B7 CRC64;

Query Match 34.8%; Score 16; DB 1; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.6e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FPELW 8
DB 5 FSLDVM 10

RESULT 12
CA42 LITCI
ID CA42 LITCI STANDARD; PRT; 11 AA.
AC P82092;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 4.2/4.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue

```


RT maintains tree frog litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SURCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 32.6%; Score 15; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFF 4
 DB 6 GSHF 9

RESULT 13

ID CXAZ_CONGE STANDARD; PRT; 13 AA.
 AC P01520;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin GII.
 OS Conus geographus (Geography cone).
 OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.

RA MEDLINE=81191854; PubMed=7014556;
 RX Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;
 RT "Peptide toxins from Conus geographus venom."
 RL J. Biol. Chem. 256:4734-4740(1981).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=84280842; PubMed=6466616;
 RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,
 RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
 RA Cruz L.J., Rivier J.;
 RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of iodinated derivatives."
 RL Biochemistry 23:2796-2802(1984).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they bind to the nicotinic acetylcholine receptors (nAChR) and thus inhibit them.
 CC -!- SURCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type family.
 DR PIR; A01783; NTKN2G.
 DR HSP; P56973; 1B45.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 7
 FT DISULFID 3 13
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1422 MW; DEE8831C39297BED CRC64;

Query Match 32.6%; Score 15; DB 1; Length 13;

Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GSFFS 5
 DB 8 GKHS 12

RESULT 14

KARA BROPL
 ID KARA BROPL STANDARD; PRT; 14 AA.
 AC P22442;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Karatasin (EC 3.4.22.-) (Fragment).
 OS Bromelia plumieri (Karatasi).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
 OC Bromelia.
 OX NCBI_TaxID=4617;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90344224; PubMed=1368518;
 RA Montes C., Amador M., Cuevas D., Cordoba F.;
 RT "Subunit structure of karatasin, the proteinase isolated from Bromelia plumieri (karatasi)."
 RL Agric. Biol. Chem. 54:17-24(1990).
 CC -!- SUBUNIT: Dimer of two small subunits linked by disulfide bonds.
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 DR PIR; PT0029; PT0029.
 DR InterPro; IPR000169; SHprot_acsite.
 DR PROSITE; PS00139; THIOL_PROTEASE_C1S; PARTIAL.
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1602 MW; FDA156893F0834PA CRC64;

Query Match 32.6%; Score 15; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.2e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 ELW 8
 DB 3 ETW 5

RESULT 15

CORZ_PERAM
 ID CORZ_PERAM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach."
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
 CC -!- SURCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.

KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FSELM 8
: | |
Db 5 YSRGW 9

Search completed: September 20, 2004, 17:31:08
Job time : 10 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 20, 2004, 17:29:05 ; Search time 15 Seconds
(without alignments)
51.302 Million cell updates/sec

Title: AUDET-SEQ1

Perfect score: 46

Sequence: 1 gffselw 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1421

Minimum DB seq length: 11

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: piri:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	50.0	15	2 PH1613	Ig H chain V-D-J r
2	22	47.8	15	2 F29501	fibrinopeptide A -
3	20	43.5	13	2 S32473	lymnaeFamide 3 - g
4	20	43.5	13	2 H56046	urinary tract ston
5	19	41.3	15	2 I29501	fibrinopeptide A -
6	19	41.3	15	2 S43956	Ig mu chain V regi
7	18	39.1	11	1 LFTWWE	probable trypsin lea
8	18	39.1	11	2 S33300	probable substance
9	18	39.1	14	2 A17150	Glucose 1-dehydrog
10	18	39.1	15	2 PH1366	Ig heavy chain DJ
11	17	37.0	12	2 PH1189	T-cell receptor al
12	17	37.0	12	2 PH1180	T-cell receptor al
13	17	37.0	12	2 PH1183	T-cell receptor al
14	17	37.0	12	2 PH1188	T-cell receptor al
15	17	37.0	12	2 PH1172	T-cell receptor al
16	17	37.0	12	2 PH1175	T-cell receptor al
17	17	37.0	14	2 B44854	L-2,4-diaminobuty
18	17	37.0	14	2 PH1448	T-cell receptor al
19	17	37.0	14	2 PH1450	T-cell receptor al
20	17	37.0	14	2 PH0945	T-cell receptor be
21	17	37.0	15	2 S26516	T-cell receptor al
22	17	37.0	15	2 S26524	T-cell receptor al
23	17	37.0	15	2 S26527	T-cell receptor al
24	17	37.0	15	2 S26528	T-cell receptor al
25	17	37.0	15	2 S26534	T-cell receptor al
26	17	37.0	15	2 PH1436	T-cell receptor al
27	16.5	35.9	15	2 PH1365	Ig heavy chain DJ
28	16	34.8	11	2 CS3652	rhlR protein - Pse
29	16	34.8	11	2 PT0302	Ig heavy chain CRD

gene HEXA protein
Ig heavy chain CRD
Ig heavy chain DJ
Ig heavy chain DJ
aggreca - bovine
T-cell receptor be
glutamine-tRNA lig
collecting duct wa
somatostatin - spo
alpha-conotoxin Cn
hypothetical prote
S-allele-associate
Ig heavy chain DJ
translation elonga
fructose-bisphosph
chromogranin-B - r

ALIGNMENTS

RESULT 1

PH1613

Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1613

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1613

A;Molecule type: DNA

A;Residues: 1-15 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 50.0%; Score 23; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 3.2e+02;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FFESEIW 8

Db 9 YFTMLW 14

RESULT 2

F29501

fibrinopeptide A - wombat

C;Species: Vombatidae gen. sp. (wombat)

C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000

C;Accession: F29501

R;Blombaeck, B.; Blombaeck, M.; Hann, C.

unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Se:

A;Reference number: A29501

A;Accession: F29501

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BLQ>

C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 47.8%; Score 22; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSPFSE 6

Db 5 GSFLAE 10

RESULT 3

S32473

lymnaeFamide 3 - great pond snail

C;Species: *Lymnaea stagnalis* (great pond snail)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
 C;Accession: S32473
 R;Johnsen, A.H.; Rehfeld, J.F.
 Eur. J. Biochem. 213, 875-879, 1993
 A;Title: *Lymnaea* Faminides, a new family of neuropeptides from the pond snail, *Lymnaea stagnalis*
 A;Reference number: S32471; MUID:93238777; PMID:8477756
 A;Accession: S32473
 A;Molecule type: protein
 A;Residues: 1-13 <JOH>
 A;Cross-references: PIDN:AAB26364.1; PID:g299831
 A;Experimental source: ganglia
 C;Keywords: amidated carboxyl end; neuropeptide
 F;11/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 43.5%; Score 20; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSPFSE 6
 |||||
 Db 7 GSAFSD 12

RESULT 4

H56046
 urinary tract stone matrix protein 10, 42K - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995
 C;Accession: H56046
 R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
 submitted to the Protein Sequence Database, February 1995
 A;Description: Isolation, characterization and sequence of stone proteins.
 A;Reference number: A56046
 A;Accession: H56046
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <BIN>

Query Match 43.5%; Score 20; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SFRSEL 7
 ||:|:|
 Db 3 SYFNDL 8

RESULT 5

I29501
 fibrinopeptide A - kangaroo
 C;Species: *Macropus* sp. (kangaroo)
 C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
 C;Accession: I29501
 R;Blomback, B.; Blomback, M.; Hann, C.
 unpublished results, cited by Blomback, B., and Blomback, M., in *Chemotaxonomy and Serology of the Macropodidae*, 1987
 A;Reference number: A29501
 A;Accession: I29501
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-15 <BLO>
 C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 41.3%; Score 19; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSPFSE 6
 ||:|:|
 Db 5 GTFIAP 10

RESULT 6

S43956
 Ig mu chain V region (clone 17) - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
 C;Accession: S43956
 R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.
 Nucleic Acids Res. 22, 1389-1393, 1994
 A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
 A;Reference number: S43956; MUID:94248036; PMID:8190629
 A;Accession: S43956
 A;Molecule type: DNA
 A;Residues: 1-15 <WAG>
 C;Keywords: immunoglobulin

Query Match 41.3%; Score 19; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

Qy 1 GSPFSELW 8
 |||||
 Db 7 GSP--DWM 12

RESULT 7

LPTWWE
 Probable trpEG leader peptide - *Thermus aquaticus*
 C;Species: *Thermus aquaticus*
 C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
 C;Accession: S03315
 R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
 Biochim. Biophys. Acta 950, 303-312, 1988
 A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and trpEG genes.
 A;Reference number: S03315; MUID:89000781; PMID:2844259
 A;Accession: S03315
 A;Molecule type: DNA
 A;Residues: 1-11 <SAT>
 A;Cross-references: EMBL:X07744; NID:G48261; PIDN:CAA30565.1; PID:G48262
 A;Note: the source is designated as *Thermus thermophilus* HB8
 C;Genetics:
 A;Gene: trpL
 C;Superfamily: probable trpEG leader peptide

Query Match 39.1%; Score 18; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SELW 8
 |||||
 Db 5 SALW 8

RESULT 8

S33300
 probable substance P - smaller spotted catshark
 C;Species: *Scyliorhinus canicula* (smaller spotted catshark, smaller spotted dogfish)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
 C;Accession: S33300
 R;Wang, D.; Wang, Y.; Hazon, N.; Balmont, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993
 A;Title: Primary structures and biological activities of substance-P-related peptides f
 A;Reference number: S33300; MUID:93292508; PMID:7685693
 A;Accession: S33300
 A;Molecule type: protein
 A;Residues: 1-11 <WAU>
 A;Experimental source: brain
 C;Function:
 A;Description: may play a physiological role in the regulation of cardiovascular and ga
 A;Note: substance P is derived by post-translational processing of preprotachykinin A
 C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 39.1%; Score 18; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFF 4
| | |
Db 5 GQFF 8

RESULT 9

AL17150
glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Jun-2002
C/Accession: AL17150
R/Franzen, B.; Carrubba, C.; Feingold, D.S.; Ashcom, J.; Franzen, J.S.
Biochem. J. 199, 599-602, 1981
A/Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol
A/Reference number: AL17150; MUID:82182061; PMID:6896145
A/Accession: AL17150
A/Molecule type: protein
A/Residues: 1-14 <FRA>
C/Keywords: NAD; oxidoreductase

Query Match 39.1%; Score 18; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSE 6
| | |
Db 7 GSCFZZ 12

RESULT 10

PH1366
IG heavy chain DJ region (clone C111-106) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1366
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1366
A/Molecule type: DNA
A/Residues: 1-15 <WAS>
C/Keywords: heterotetramer; immunoglobulin

Query Match 39.1%; Score 18; DB 2; Length 15;
Best Local Similarity 16.7%; Pred. No. 3e+03;
Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFSLEW 8
: : :
Db 6 YGDDY 11

RESULT 11

PH1189
T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1189
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1189
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSFFSEL 7
| | | |
Db 6 GGFASAL 12

RESULT 12

PH1180
T-cell receptor alpha chain V region (Cw3/5B8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1180
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1180
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSFFSEL 7
| | | |
Db 6 GGFASAL 12

RESULT 13

PH1183
T-cell receptor alpha chain V region (Cw3/3A8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1183
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1183
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSFFSEL 7
| | | |
Db 6 GGFASAL 12

RESULT 14

PH1188
T-cell receptor alpha chain V region (Cw3/Cas11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1188
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1188
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSPFSEL 7
| | | |
Db 6 GGFASAL 12

RESULT 15
PH1172
T-cell receptor alpha chain V region (Cw3/Cas15) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1172
R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH1172
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>

Query Match 37.0%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSPFSEL 7
| | | |
Db 6 GGFASAL 12

Search completed: September 20, 2004, 17:32:10
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:59 ; Search time 122 Seconds
(without alignments)
23.160 Million cell updates/sec

Title: AUDT681-1
Perfect score: 55
Sequence: 1 gsfsselwts 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 532682

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	12	4	AAB86005 DCM-assoc
2	55	100.0	13	4	AAB86006 DCM-assoc
3	55	100.0	14	4	AAB86012 DCM-assoc
4	55	100.0	14	4	AAB86020 DCM-assoc
5	55	100.0	15	4	AAB86013 DCM-assoc
6	55	100.0	15	4	AAB86021 DCM-assoc
7	34	61.8	8	3	AAB09130 Hepatitis
8	34	61.8	18	5	AAB091098 Human sec
9	34	61.8	18	5	AAB091081 Human sec
10	34	61.8	18	5	ABG65209 Human alb
11	34	61.8	18	5	ABG65210 Human alb
12	33	60.0	13	4	AAB86007 DCM-assoc
13	33	60.0	15	4	AAB86014 DCM-assoc
14	33	60.0	15	4	AAB86022 DCM-assoc
15	33	60.0	15	5	AAB020307 Human ple
16	30	54.5	6	6	ABR46515 Staphyloc
17	30	54.5	9	2	AAW72493 Dengue vi
18	30	54.5	10	2	AAW37198 Human onc
19	30	54.5	13	4	AAB86009 DCM-assoc
20	30	54.5	13	5	AAW47221 Dilated c
21	30	54.5	14	2	AAW50952 Somatosta
22	30	54.5	14	4	AAB91005 Somatosta
23	30	54.5	15	4	AAB86028 DCM-assoc
24	30	54.5	15	4	AAB86017 DCM-assoc
25	30	54.5	22	4	AAW15937 Peptide #

ALIGNMENTS

RESULT 1
AAB86005
ID AAB86005 standard; peptide; 12 AA.

XX AAB86005;
XX AC
XX 12-JUL-2001 (first entry)
XX DCM-associated peptide #5.
XX DCM; dilative cardiomyopathy; autoantibody; cardiant;
KW beta-1 adrenergic activated antibody; immunosuppressive.
XX Synthetic.
XX WO200121660-A1.
XX 29-MAR-2001.
XX 21-SEP-2000; 2000WO-EP009241.
XX 21-SEP-1999; 99EP-00118630.
XX 21-SEP-1999; 99EP-00118631.
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX WPI; 2001-335469/35.
XX New peptide useful for combating the autoantibodies that are responsible
XX for dilative cardiomyopathy.
XX Claim 3; Page 20; 29pp; German.
XX This invention describes a novel peptide (PI) which can be used for (1)
XX isolating beta-1 adrenergic activated antibodies bound to (PI) on a solid
XX phase; and (2) a chromatographic apparatus with (PI) bound. The products
XX of the invention have cardiant and immunosuppressive activity. (PI) is
XX used to produce medicine to combat beta 1 adrenergic activated
XX autoantibodies having a causal pathological relationship with dilative
XX cardiomyopathy. This sequence represents a specifically claimed peptide
XX used to illustrate the method of the invention

Sequence 12 AA;

Query Match 100.0%; Score 55; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.004;

Abb34927 Peptide #
Aam28440 Peptide #
Abb29754 Peptide #
Abb20338 Protein #
Aam68116 Human bra
Aam55735 Human bra
Abg49763 Human liv
Aam03673 Peptide #
Abg37639 Human pep
Aay33139 Rabbit ca
Aau93215 Granulocy
Abj37125 Rhodopsin
Abj37231 Rhodopsin
Aae39001 Human RAT
Aay36456 Fragment
Ada11991 Human nov
Aar70670 Transmembr
Abr46459 Staphyloc
Aay04678 Peptide #
Abb55959 Vascular

26 30 54.5 22 4 ABB34927
27 30 54.5 22 4 AAM28440
28 30 54.5 22 4 ABB29754
29 30 54.5 22 4 ABB20338
30 30 54.5 22 4 AAM68116
31 30 54.5 22 4 AAM55735
32 30 54.5 22 4 ABG49763
33 30 54.5 22 4 AAM03673
34 30 54.5 22 5 ABG37639
35 29 52.7 7 2 AAY33139
36 29 52.7 10 5 AAU93215
37 29 52.7 11 6 ABJ37125
38 29 52.7 15 6 ABJ37231
39 29 52.7 16 7 AAE39001
40 29 52.7 21 2 AAY36456
41 29 52.7 21 6 ADA11991
42 29 52.7 22 2 AAR70670
43 28 50.9 6 6 ABR46459
44 28 50.9 9 2 AAY04678
45 28 50.9 10 4 ABB55959

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELTWS 10
Db 1 GSFFSELTWS 11
2 GSFFSELTWS 11

RESULT 2
AAB86006
ID AAB86006 standard; peptide; 13 AA.
XX AC
XX AAB86006;
DT 12-JUL-2001 (first entry)
XX AC
DE DCM-associated peptide #6.
XX DCM; dilatative cardiomyopathy; autoantibody; cardiant;
KW beta-1 adrenergic activated antibody; immunosuppressive.
KW Synthetic.
OS
XX WO200121660-A1.
PN
XX 29-MAR-2001.
PD
XX 21-SEP-2000; 2000WO-EP009241.
PF
XX 21-SEP-1999; 99EP-00118630.
PR 21-SEP-1999; 99EP-00118631.
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX PA
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
PI WPI; 2001-335469/35.
DR
XX New peptide useful for combating the autoantibodies that are responsible
PT for dilatative cardiomyopathy.
PT
XX Claim 3; Page 21; 29pp; German.
PS
XX This invention describes a novel peptide (P1) which can be used for (1)
CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
CC of the invention have cardiant and immunosuppressive activity. (P1) is
CC used to produce medicine to combat beta_1 adrenergic activated
CC autoantibodies having a causal pathological relationship with dilatative
CC cardiomyopathy. This sequence represents a specifically claimed peptide
CC used to illustrate the method of the invention
XX
XX Sequence 13 AA;
SQ
Query Match 100.0%; Score 55; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELTWS 10
Db 3 GSFFSELTWS 12

RESULT 3
AAB86012
ID AAB86012 standard; peptide; 14 AA.
XX AC
XX AAB86012;
DT 12-JUL-2001 (first entry)
XX AC
DE DCM-associated peptide #12.
XX DCM; dilatative cardiomyopathy; autoantibody; cardiant;
KW

```

```

KW beta-1 adrenergic activated antibody; immunosuppressive.
XX Synthetic.
OS
XX Key Location/Qualifiers
PH Modified-site 14
FT /note= "Lys modified with an amide or free acid group"
XX
XX WO200121660-A1.
PN
XX 29-MAR-2001.
PD
XX 21-SEP-2000; 2000WO-EP009241.
PF
XX 21-SEP-1999; 99EP-00118630.
PR 21-SEP-1999; 99EP-00118631.
XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX PA
XX Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
PI WPI; 2001-335469/35.
DR
XX New peptide useful for combating the autoantibodies that are responsible
PT for dilatative cardiomyopathy.
PT
XX Claim 4; Page 22; 29pp; German.
PS
XX This invention describes a novel peptide (P1) which can be used for (1)
CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
CC of the invention have cardiant and immunosuppressive activity. (P1) is
CC used to produce medicine to combat beta_1 adrenergic activated
CC autoantibodies having a causal pathological relationship with dilatative
CC cardiomyopathy. This sequence represents a specifically claimed peptide
CC used to illustrate the method of the invention
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 55; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFSELTWS 10
Db 2 GSFFSELTWS 11

RESULT 4
AAB86020
ID AAB86020 standard; peptide; 14 AA.
XX AC
XX AAB86020;
DT 12-JUL-2001 (first entry)
XX AC
DE DCM autoantibody-associated peptide #1.
XX DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
KW autoantibody; myocardial.
XX Synthetic.
OS
XX Key Location/Qualifiers
PH Modified-site 1
FT /note= "N-terminal acetylated"
XX Modified-site 14
FT /note= "C-terminal amide"
XX
XX DEL19945211-A1.
PN
XX 29-MAR-2001.
PD
XX

```


PF 21-SEP-1999; 99DE-01045211.
 XX
 PR 21-SEP-1999; 99DE-01045211.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX WPI; 2001-301259/32.
 DR
 XX
 XX New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a beta1-adrenergic receptor group useful for treating
 PT dilatative cardiomyopathy.
 XX
 PS Claim 2; Page 5; 8pp; German.
 XX
 XX This invention describes novel peptides (I) with an amino acid sequence
 CC corresponding a beta1-adrenergic receptor group recognized by
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
 CC invention also describes a chromatographic device comprising (I) bound to
 CC a solid phase. The products of the invention have cardiant activity. (I)
 CC are useful for treating DCM by binding autoantibodies directed against
 CC myocardial beta1-adrenergic receptors, either by neutralizing the
 CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
 CC (I) immobilized on a solid phase. This sequence represents a specifically
 CC claimed peptide used to illustrate the method of the invention
 XX
 SQ Sequence 14 AA;

 Query Match 100.0%; Score 55; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GSFFSELWTS 10
 DB 2 GSFFSELWTS 11

 RESULT 5
 AAB86013
 ID AAB86013 standard; peptide; 15 AA.
 XX
 AC AAB86013;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM-associated peptide #13.
 XX
 KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
 KW beta-1 adrenergic activated antibody; immunosuppressive.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 15
 FT /note= "Lys modified with an amide or free acid group"
 XX
 PN WO200121660-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-EP009241.
 XX
 PR 21-SEP-1999; 99EP-00118630.
 PR 21-SEP-1999; 99EP-00118631.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX WPI; 2001-335469/35.
 DR
 XX New peptide useful for combating the autoantibodies that are responsible

PT for dilatative cardiomyopathy.
 XX
 PS Claim 4; Page 22; 29pp; German.
 XX
 CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilatative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention
 XX
 SQ Sequence 15 AA;

 Query Match 100.0%; Score 55; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GSFFSELWTS 10
 DB 3 GSFFSELWTS 12

 RESULT 6
 AAB86021
 ID AAB86021 standard; peptide; 15 AA.
 XX
 AC AAB86021;
 XX
 DT 12-JUL-2001 (first entry)
 XX
 DE DCM autoantibody-associated peptide #2.
 XX
 KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
 KW autoantibody; myocardial.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetylated"
 FT Modified-site 15
 FT /note= "C-terminal amide"
 XX
 PN DE19945211-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-1999; 99DE-01045211.
 XX
 PR 21-SEP-1999; 99DE-01045211.
 XX
 PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX
 PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX WPI; 2001-301259/32.
 DR
 XX New autoantibody-binding peptides with an amino acid sequence
 PT corresponding a beta1-adrenergic receptor group useful for treating
 PT dilatative cardiomyopathy.
 XX
 PS Claim 2; Page 5; 8pp; German.
 XX
 CC This invention describes novel peptides (I) with an amino acid sequence
 CC corresponding a beta1-adrenergic receptor group recognized by
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
 CC invention also describes a chromatographic device comprising (I) bound to
 CC a solid phase. The products of the invention have cardiant activity. (I)
 CC are useful for treating DCM by binding autoantibodies directed against
 CC myocardial beta1-adrenergic receptors, either by neutralizing the
 CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
 CC antibodies

CC (1) immobilized on a solid phase. This sequence represents a specifically
 CC claimed peptide used to illustrate the method of the invention

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 55; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSPFSELWTS 10
 |||||
 Db 3 GSPFSELWTS 12

RESULT 7
 AAB09130
 ID AAB09130 standard; protein; 8 AA.
 XX
 AC AAB09130;
 XX
 DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (first entry)
 XX
 DE Hepatitis GB virus protein sequence SEQ ID NO:252.
 XX
 KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.
 XX
 OS Hepatitis GB virus.
 XX
 PN US6051374-A.
 XX
 PD 18-APR-2000.
 XX
 PF 07-JUN-1995; 95US-00489445.
 XX
 PR 14-FEB-1994; 94US-00196030.
 PR 13-MAY-1994; 94US-00242654.
 PR 23-JUL-1994; 94US-00283314.
 PR 23-NOV-1994; 94US-00344185.
 PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-00377557.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Bui'k SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX
 DR WPI; 2000-338307/29.

XX Detecting target hepatitis GB virus nucleic acid in a test sample
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX
 XX Example 9; Col 331-332; 369pp; English.

XX The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which
 CC selectively hybridises to the HGBV genome or its full complement, and
 CC detecting the complex that contains THN, indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -E hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and
 CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 8 AA;

Query Match 61.8%; Score 34; DB 3; Length 8;

Best Local Similarity 85.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 FSELWTS 10
 |||||
 Db 1 FSHLWTS 7

RESULT 8
 AAU91098
 ID AAU91098 standard; protein; 18 AA.
 XX
 AC AAU91098;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human secreted protein sequence #18.
 XX
 KW Human secreted protein; autoimmune disease; hyperproliferative disorder;
 KW cardiovascular disorder; cerebrovascular disorder; infection; cancer;
 KW nervous system disorder; ocular disorder; epithelial cell proliferation;
 KW wound healing; skin aging; sunburn; transplantation; chemotaxis;
 KW tissue regeneration; food additive; preservative; cytostatic; cardiant;
 KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.
 XX
 OS Homo sapiens.
 XX
 PN WO200218412-A1.
 XX
 PD 07-MAR-2002.
 XX
 PF 17-JAN-2001; 2001WO-US001384.
 XX
 PR 28-AUG-2000; 2000US-0228086P.
 PR 04-JAN-2001; 2001US-0259516P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;
 PI Fiscella M, Ni J;
 XX
 DR WPI; 2002-269525/31.
 DR N-PSDB; ABK54136.

XX Seventeen nucleic acid molecules encoding human secreted proteins, useful
 PT in the prevention, treatment and diagnosis of cancer, immune disorders,
 PT cardiovascular disorders and neurological diseases.

PS Claim 11; Page 461; 505pp; English.

XX The present invention relates to the isolation of novel human secreted
 CC proteins, and the polynucleotide sequences encoding them. The secreted
 CC proteins are useful to prevent, treat or ameliorate a medical condition
 CC in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or
 CC sheep. The secreted proteins are also useful in diagnosing a pathological
 CC condition or susceptibility to a pathological condition. Antibodies to
 CC the secreted proteins can also be used in alleviating symptoms associated
 CC with disorders and in diagnostic immunoassays e.g. radioimmunoassays or
 CC enzyme linked immunosorbent assays (ELISA). Disorders which can be
 CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. cancer, cardiovascular
 CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
 CC ischaemia, angiogenesis, nervous system disorders e.g. Parkinson's
 CC disease, infections caused by bacteria, viruses and fungi and ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. AAU91081-
 CC AAU91148 represent human secreted protein sequences

SQ Sequence 18 AA; Query Match 61.8%; Score 34; DB 5; Length 18; Best Local Similarity 85.7%; Pred. No. 34; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FSELWTS 10
 ||| |||
 3 FSEAWTS 9

Db 3 FSEAWTS 9

RESULT 9
 AAU91081
 ID AAU91081 standard; protein; 18 AA.
 XX
 AC AAU91081;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human secreted protein sequence #1.
 XX
 KW Human secreted protein; autoimmune disease; hyperproliferative disorder;
 KW cardiovascular disorder; cerebrovascular disorder; infection; cancer;
 KW nervous system disorder; ocular disorder; epithelial cell proliferation;
 KW wound healing; skin aging; sunburn; transplantation; chemotaxis;
 KW tissue regeneration; food additive; preservative; cytostatic; cardiant;
 KW antiviral; antiallergic; antiinflammatory; antibacterial; antifungal.
 XX
 OS Homo sapiens.
 XX
 FN WO200218412-A1.
 XX
 PD 07-MAR-2002.
 XX
 PF 17-JAN-2001; 2001WO-US001384.
 XX
 PR 28-AUG-2000; 2000US-0228086P.
 PR 04-JAN-2001; 2001US-0259516P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR;
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan RD, Shi Y, Choi GH;
 PI Fiscella M, Ni J;
 XX
 DR WPI; 2002-269525/31.
 DR N-PSDB; ABR54119.
 XX
 PT Seventeen nucleic acid molecules encoding human secreted proteins, useful
 PT in the prevention, treatment and diagnosis of cancer, immune disorders,
 PT cardiovascular disorders and neurological diseases.
 XX
 PS Claim 11; Page 450; 505pp; English.
 XX
 CC The present invention relates to the isolation of novel human secreted
 CC proteins, and the polynucleotide sequences encoding them. The secreted
 CC proteins are useful to prevent, treat or ameliorate a medical condition
 CC in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or
 CC sheep. The secreted proteins are also useful in diagnosing a pathological
 CC condition or susceptibility to a pathological condition. Antibodies to
 CC the secreted proteins can also be used in alleviating symptoms associated
 CC with disorders and in diagnostic immunoassays e.g. radioimmunoassays or
 CC enzyme linked immunosorbent assays (ELISA). Disorders which can be
 CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
 CC arthritis, hyperproliferative disorders e.g. cancer, cardiovascular
 CC disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral
 CC ischaemia, angiogenesis, nervous system disorders e.g. Parkinson's
 CC disease, infections caused by bacteria, viruses and fungi and ocular
 CC disorders e.g. corneal infection. The polypeptides can also be used to
 CC aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or

CC preservative to increase or decrease storage capabilities. AAU91081-
 CC AAU91148 represent human secreted protein sequences

SQ Sequence 18 AA; Query Match 61.8%; Score 34; DB 5; Length 18; Best Local Similarity 85.7%; Pred. No. 34; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FSELWTS 10
 ||| |||
 3 FSEAWTS 9

Db 3 FSEAWTS 9

RESULT 10
 ABG65209
 ID ABG65209 standard; protein; 18 AA.
 XX
 AC ABG65209;
 XX
 DT 27-AUG-2002 (first entry)
 XX
 DE Human albumin fusion protein #1884.
 XX
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; antiinfertility; antiinflammatory; antiulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200177137-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-US011988.
 XX
 PR 12-APR-2000; 2000US-0229358P.
 PR 25-APR-2000; 2000US-019384P.
 PR 21-DEC-2000; 2000US-0258931P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Haseltine WA;
 XX
 DR WPI; 2002-010886/01.
 XX
 PT New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 XX
 PS Claim 1; Page 1828; 2102pp; English.
 XX
 CC The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX
 SQ Sequence 18 AA;

```

Query Match      61.8%; Score 34; DB 5; Length 18;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FSELWTS 10
Db 3 FSEAWTS 9
    ||| |||
    3 FSEAWTS 9

RESULT 11
ABG65210
ID ABG65210 standard; protein; 18 AA.
XX AC ABG65210;
XX DT 27-AUG-2002 (first entry)
XX DE Human albumin fusion protein #1885.
XX KW Albumin fusion protein; therapeutic protein X; human albumin; HA;
XX KW human serum albumin; HSA; cancer; reproductive disorder;
XX KW digestive disorder; immune disorder; endocrine disorder;
XX KW haematopoietic disorder; neural disorder; connective disorder;
XX KW cytostatic; antifertility; antiinflammatory; antiulcer;
XX KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
XX KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
XX KW osteopathic; antiarthritic.
OS Homo sapiens.
OS Synthetic.
XX PN WO200177137-A1.
XX PD 18-OCT-2001.
XX PF 12-APR-2001; 2001WO-US011988.
XX PR 12-APR-2000; 2000US-0229358P.
XX PR 25-APR-2000; 2000US-0199384P.
XX PR 21-DEC-2000; 2000US-0256931P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Haseltine WA;
XX DR WPI; 2002-010886/01.
XX PT New fusion protein for treating disease e.g. diabetes comprises an
    PT albumin fused to a therapeutic protein.
XX PS Claim 1; Page 1828; 2102pp; English.
XX CC The present invention relates to albumin fusion proteins comprising a
    CC therapeutic protein X and human albumin (HA, also known as human serum
    CC albumin, HSA). The proteins are useful for treating a disease or disorder
    CC that may be modulated by therapeutic protein X. The albumin extends the
    CC shelf-life of protein X, and may increase its biological in vitro/in vivo
    CC activity. The protein is useful for treating and diagnosing disorders
    CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
    CC disease, ulcerative colitis), immune disorders (e.g. acquired
    CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
    CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
    CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
    CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
    CC ABG63326-ABG6518 represent albumin fusion proteins of the invention
    CC
    CC Sequence 18 AA;
    CC
Query Match      61.8%; Score 34; DB 5; Length 18;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 FSELWTS 10
Db 3 FSEAWTS 9
    ||| |||
    3 FSEAWTS 9

RESULT 12
AAB86007
ID AAB86007 standard; peptide; 13 AA.
XX AC AAB86007;
XX DT 12-JUL-2001 (first entry)
XX DE DCM-associated peptide #7.
XX KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
    KW beta-1 adrenergic activated antibody; immunosuppressive.
XX OS Synthetic.
XX PN WO200121660-A1.
XX PD 29-MAR-2001.
XX PF 21-SEP-2000; 2000WO-EP009241.
XX PR 21-SEP-1999; 99EP-00118630.
XX PR 21-SEP-1999; 99EP-00118631.
XX PA (AFFI-) AFFINA IMMUNOTECHNIK GMBH.
XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
XX DR WPI; 2001-335469/35.
XX PT New peptide useful for combating the autoantibodies that are responsible
    PT for dilatative cardiomyopathy.
XX PS Claim 3; Page 21; 29pp; German.
XX CC This invention describes a novel peptide (P1) which can be used for (1)
    CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
    CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
    CC of the invention have cardiant and immunosuppressive activity. (P1) is
    CC used to produce medicine to combat beta 1 adrenergic activated
    CC autoantibodies having a causal pathological relationship with dilatative
    CC cardiomyopathy. This sequence represents a specifically claimed peptide
    CC used to illustrate the method of the invention
    CC
    CC Sequence 13 AA;
    CC
Query Match      60.0%; Score 33; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 GSFFSELWTS 10
Db 3 GTLFSDFWLS 12
    | : | : | : |
    3 GTLFSDFWLS 12

RESULT 13
AAB86014
ID AAB86014 standard; peptide; 15 AA.
XX AC AAB86014;
XX DT 12-JUL-2001 (first entry)
XX DE DCM-associated peptide #14.
XX KW DCM; dilatative cardiomyopathy; autoantibody; cardiant;
    KW beta-1 adrenergic activated antibody; immunosuppressive.
XX OS Synthetic.

```

XX FH Key Location/Qualifiers
 XX FT Modified-site 15
 XX FT /note= "Lys modified with an amide or free acid group"
 XX PN WO200121660-A1.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-2000; 2000WO-EF009241.
 XX PR 21-SEP-1999; 99EP-00118630.
 XX PR 21-SEP-1999; 99EP-00118631.
 XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX PI MPI; 2001-335469/35.
 XX DR New peptide useful for combating the autoantibodies that are responsible
 XX PT for dilatative cardiomyopathy.
 XX PS Claim 4; Page 22; 29pp; German.
 XX CC This invention describes a novel peptide (P1) which can be used for (1)
 CC isolating beta-1 adrenergic activated antibodies bound to (P1) on a solid
 CC phase; and (2) a chromatographic apparatus with (P1) bound. The products
 CC of the invention have cardiant and immunosuppressive activity. (P1) is
 CC used to produce medicine to combat beta-1 adrenergic activated
 CC autoantibodies having a causal pathological relationship with dilatative
 CC cardiomyopathy. This sequence represents a specifically claimed peptide
 CC used to illustrate the method of the invention
 XX SQ Sequence 15 AA;

Query Match 60.0%; Score 33; DB 4; Length 15;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GSFFSELWTS 10
 DB 3 GTLFSDFWLS 12
 RESULT 14
 ID AAB86022 standard; peptide; 15 AA.
 AC AAB86022;
 DT 12-JUL-2001 (first entry)
 DE DCM autoantibody-associated peptide #3.
 KW DCM; dilatative cardiomyopathy; beta-1-adrenergic receptor; cardiant;
 KW autoantibody; myocardial.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1
 XX FT /note= "N-terminal acetylated"
 XX FT Modified-site 15
 XX FT /note= "C-terminal amide"
 XX PN DE19945211-A1.
 XX PD 29-MAR-2001.
 XX PF 21-SEP-1999; 99DE-01045211.
 XX PR 21-SEP-1999; 99DE-01045211.

XX PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
 XX PI Roenspeck W, Kunze R, Wallukat G, Dierenfeld M;
 XX PI MPI; 2001-301259/32.
 XX DR New autoantibody-binding peptides with an amino acid sequence
 XX PT corresponding a beta-1-adrenergic receptor group useful for treating
 XX PT dilatative cardiomyopathy.
 XX PS Claim 2; Page 5; 8pp; German.
 XX CC This invention describes novel peptides (I) with an amino acid sequence
 CC corresponding a beta-1-adrenergic receptor group recognized by
 CC autoantibodies associated with dilatative cardiomyopathy (DCM). The
 CC invention also describes a chromatographic device comprising (I) bound to
 CC a solid phase. The products of the invention have cardiant activity. (I)
 CC are useful for treating DCM by binding autoantibodies directed against
 CC myocardial beta-1-adrenergic receptors, either by neutralizing the
 CC antibodies in vivo or by extracorporeal treatment of blood or plasma with
 CC (I) immobilized on a solid phase. This sequence represents a specifically
 CC claimed peptide used to illustrate the method of the invention
 XX SQ Sequence 15 AA;
 Query Match 60.0%; Score 33; DB 4; Length 15;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GSFFSELWTS 10
 DB 3 GTLFSDFWLS 12
 RESULT 15
 ID AAO20307 standard; peptide; 15 AA.
 AC AAO20307;
 DT 31-MAY-2002 (first entry)
 DE Human plectin 10 protein N-terminal region.
 KW Human; plectin 10; DNA recombination; cancer; HIV infection.
 OS Homo sapiens.
 XX CN1325901-A.
 XX PD 12-DEC-2001.
 XX PF 31-MAY-2000; 2000CN-00116269.
 XX PR 31-MAY-2000; 2000CN-00116269.
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX PI Mao Y, Xie Y;
 XX PI MPI; 2002-196661/26.
 XX PT Polypeptide-human plectin 10 and polynucleotide encoding it.
 XX PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
 XX CC The invention relates to the novel polypeptide-human plectin 10, the
 CC polynucleotide encoding it, the process for preparing the polypeptide by
 CC DNA recombination, the application of the polypeptide in treating
 CC diseases such as cancer and HIV infection. The invention also relates to
 CC the antagonist of the polypeptide and its medical action, and the
 CC application of the polynucleotide. This sequence represents an N-terminal

```
CC  region of the human plectin 10 protein of the invention
XX
SQ  Sequence 15 AA;
    Query Match      60.0%; Score 33; DB 5; Length 15;
    Best Local Similarity 55.6%; Pred. No. 42;
    Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY  2 SPFSELWTS 10
    :|||:|
Db  2 APFSSIWLS 10

Search completed: August 27, 2004, 09:25:43
Job time : 127 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:22:53 ; Search time 31 seconds
(without alignments)
16.654 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gffselslws 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 186303

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	34	61.8	8	4	US-08-469-260A-252
2	34	61.8	8	4	US-08-488-446-252
3	34	61.8	8	4	US-08-467-344A-252
4	31	56.4	18	2	US-08-934-915-125
5	30	54.5	6	1	US-08-424-957-6
6	30	54.5	6	3	US-09-035-686-6
7	30	54.5	11	1	US-08-424-957-42
8	30	54.5	11	3	US-09-035-686-42
9	30	54.5	19	4	US-09-081-975-13
10	28	50.9	11	3	US-09-186-958-6
11	28	50.9	11	3	US-09-669-271A-6
12	28	50.9	11	4	US-09-881-276-6
13	28	50.9	13	2	US-08-637-759B-388
14	28	50.9	13	3	US-08-871-355A-388
15	28	50.9	13	4	US-09-201-945-388
16	27	49.1	6	1	US-08-277-660A-2
17	27	49.1	6	1	US-08-424-957-2
18	27	49.1	6	3	US-09-035-686-2
19	27	49.1	6	4	US-09-081-975-1
20	27	49.1	6	4	US-09-428-082B-130
21	27	49.1	7	1	US-08-277-660A-27
22	27	49.1	7	1	US-08-424-957-15
23	27	49.1	7	1	US-08-424-957-19
24	27	49.1	7	3	US-09-035-686-15
25	27	49.1	7	3	US-09-035-686-19
26	27	49.1	10	1	US-08-277-660A-7
27	27	49.1	10	1	US-08-424-957-11

28 27 49.1 10 1 US-08-424-957-18 Sequence 18, Appl
29 27 49.1 10 3 US-09-035-686-11 Sequence 11, Appl
30 27 49.1 10 3 US-09-035-686-18 Sequence 18, Appl
31 27 49.1 11 1 US-08-277-660A-9 Sequence 9, Appl
32 27 49.1 11 1 US-08-277-660A-10 Sequence 10, Appl
33 27 49.1 11 1 US-08-277-660A-11 Sequence 11, Appl
34 27 49.1 11 1 US-08-277-660A-12 Sequence 12, Appl
35 27 49.1 11 1 US-08-277-660A-13 Sequence 13, Appl
36 27 49.1 11 1 US-08-277-660A-19 Sequence 19, Appl
37 27 49.1 11 1 US-08-277-660A-20 Sequence 20, Appl
38 27 49.1 11 1 US-08-424-957-17 Sequence 17, Appl
39 27 49.1 11 1 US-08-424-957-23 Sequence 23, Appl
40 27 49.1 11 1 US-08-424-957-24 Sequence 24, Appl
41 27 49.1 11 1 US-08-424-957-25 Sequence 25, Appl
42 27 49.1 11 1 US-08-424-957-26 Sequence 26, Appl
43 27 49.1 11 1 US-08-424-957-32 Sequence 32, Appl
44 27 49.1 11 1 US-08-424-957-33 Sequence 33, Appl
45 27 49.1 11 1 US-08-424-957-34 Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-469-260A-252

Query Match 61.8%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10
Db 1 FSHLWTS 7

RESULT 2

US-08-488-446-252

; Sequence 252, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-488-446-252

Query Match 61.8%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10
Db 1 FSHLWTS 7

RESULT 3

US-08-488-446-252

; Sequence 252, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-488-446-252

Query Match 61.8%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10
Db 1 FSHLWTS 7

US-08-467-344A-252

; Sequence 252, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 252:

US-08-467-344A-252

Query Match 61.8%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10
Db 1 FSHLWTS 7

RESULT 4

US-08-934-915-125

; Sequence 125, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

US-08-934-915-125

Query Match 61.8%; Score 34; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSELWTS 10
Db 1 FSHLWTS 7

;; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;; NUMBER OF SEQUENCES: 193
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MASON & ASSOCIATES, P.A.
;; STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500
;; CITY: CLEARWATER
;; STATE: FLORIDA
;; COUNTRY: U.S.A.
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 3.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,915
;; FILING DATE: 22-SEP-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/949,836
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LOUISE A. FOUTCH
;; REGISTRATION NUMBER: 37,133
;; REFERENCE/DOCKET NUMBER: 1946.6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 813-538-3800
;; TELEFAX: 813-538-3820
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 125:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-934-915-125

Query Match 56.4%; Score 31; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SPFSRLWT 9
DB 5 SPFSRTWS 12

RESULT 5
US-08-424-957-6
; Sequence 6, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660

;; FILING DATE: 20-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Walter H.
;; REGISTRATION NUMBER: 24,190
;; REFERENCE/DOCKET NUMBER: A-61228/WHD
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 781-1989
;; TELEFAX: (415) 398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-08-424-957-6

Query Match 54.5%; Score 30; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
DB 2 FSELW 6

RESULT 6
US-09-035-686-6
; Sequence 6, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: PICKSLEY, STEVEN M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
US-09-035-686-6

Query Match 54.5%; Score 30; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
| | | | |
Db 2 FSELM 6

RESULT 7

US-08-424-957-42
; Sequence 42, Application US/08424957
; Patent No. 5770377
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,957
; FILING DATE: 19-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-424-957-42

Query Match 54.5%; Score 30; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
| | | | |
Db 5 FSELM 9

RESULT 8

US-09-035-686-42
; Sequence 42, Application US/09035686
; Patent No. 6153391
; GENERAL INFORMATION:
; APPLICANT: Picksley, Steven M.
; APPLICANT: Lane, David P.
; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,686
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/424,957
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: US 08/277,660
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61228/WH/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-09-035-686-42

Query Match 54.5%; Score 30; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELM 8
| | | | |
Db 5 FSELM 9

RESULT 9

US-09-081-975-13
; Sequence 13, Application US/09081975
; Patent No. 6451979
; GENERAL INFORMATION:
; APPLICANT: Kaelin, William
; APPLICANT: Jost, Christine
; TITLE OF INVENTION: METHODS OF TREATMENT USING
; TITLE OF INVENTION: NBS-1, ANTIBODIES AND PROTEINS THEREOF, AND USES OF THE
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon Peabody LLP
; STREET: 101 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,975
; FILING DATE: 12-MAY-1998
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/046,207
;; FILING DATE: 12-MAY-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eisenstein, Ronald I
;; REGISTRATION NUMBER: 30,628
;; REFERENCE/DOCKET NUMBER: 47400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-345-6054
;; TELEFAX: 617-345-1300
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-081-975-13

Query Match 54.5%; Score 30; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FSELM 8
|||
Db 8 FSELM 12

RESULT 10
US-09-186-958-6
; Sequence 6, Application US/09186958B
; Patent No. 6238860
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/186,958B
; CURRENT FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
; US-09-186-958-6

Query Match 50.9%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFSELMWS 10
|||
Db 1 FFCALWPS 8

RESULT 11
US-09-669-271A-6
; Sequence 6, Application US/09669271A
; Patent No. 6291197
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: Dyax-009.0 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/669,271A
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
;; US-09-669-271A-6

Query Match 50.9%; Score 28; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFSELMWS 10
|||
Db 1 FFCALWPS 8

RESULT 12
US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. 6479641
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Fayelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
; FILE REFERENCE: DYX-009.0 US-2
; CURRENT APPLICATION NUMBER: US/09/881,276
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/669,271
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/186,958
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypep
; US-09-881-276-6

Query Match 50.9%; Score 28; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FFSELMWS 10
|||
Db 1 FFCALWPS 8

RESULT 13
US-08-637-759B-388
; Sequence 388, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30109-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B

```
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/GB95/02875
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-637-759B-388

Query Match 50.9%; Score 28; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFSSELWTS 10
Db 3 FYSDTWLS 10

RESULT 14
US-08-871-355A-388
; Sequence 388, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/GB95/02875
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-871-355A-388

Query Match 50.9%; Score 28; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFSSELWTS 10
Db 3 FYSDTWLS 10

RESULT 15
US-09-201-945-388
; Sequence 388, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-09/201,945
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/637,759
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 388:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-09-201-945-388

Query Match 50.9%; Score 28; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFSSELWTS 10
Db 3 FYSDTWLS 10

Search completed: August 27, 2004, 09:28:43
Job time : 32 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 27, 2004, 09:26:14 ; Search time 684 Seconds
(without alignments)
4.600 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfeslwtls 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 268144

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	61.8	8	US-08-424-550B-252	Sequence 252, App
2	34	61.8	18	US-09-833-245-1958	Sequence 1958, Ap
3	34	61.8	18	US-09-833-245-1959	Sequence 1959, Ap
4	30	54.5	10	US-09-214-371-35	Sequence 35, Appl
5	30	54.5	10	US-09-214-371-36	Sequence 36, Appl
6	30	54.5	13	US-10-221-042-1	Sequence 1, Appli
7	30	54.5	19	US-10-155-059-13	Sequence 13, Appl
8	30	54.5	21	US-10-651-563-53	Sequence 53, Appl
9	30	54.5	22	US-09-864-761-35636	Sequence 35636, A
10	29	52.7	15	US-10-192-381-46	Sequence 46, Appl
11	29	52.7	16	US-10-224-356-36	Sequence 36, Appl
12	29	52.7	18	US-10-224-356-17	Sequence 17, Appl
13	29	52.7	21	US-10-372-876-519	Sequence 519, App
14	29	52.7	21	US-10-097-065-519	Sequence 519, App
15	28	50.9	9	US-09-486-734A-35	Sequence 35, Appl

16	50.9	11	9	US-09-881-276-6	Sequence 5, Appli
17	50.9	11	12	US-10-417-895A-56	Sequence 56, Appl
18	50.9	14	10	US-09-964-821B-53	Sequence 53, Appl
19	50.9	14	14	US-10-268-332-53	Sequence 53, Appl
20	50.9	16	14	US-10-225-567A-1393	Sequence 1393, Ap
21	50.9	21	9	US-09-864-761-35934	Sequence 35934, A
22	49.1	6	9	US-09-214-371-83	Sequence 83, Appl
23	49.1	6	9	US-09-732-384-4	Sequence 4, Appli
24	49.1	6	12	US-10-609-217-130	Sequence 130, App
25	49.1	6	12	US-10-632-388-130	Sequence 130, App
26	49.1	6	12	US-10-651-723-130	Sequence 130, App
27	49.1	6	12	US-10-645-761-130	Sequence 130, App
28	49.1	6	13	US-10-155-059-1	Sequence 1, Appli
29	49.1	6	16	US-10-666-696-130	Sequence 130, App
30	49.1	6	16	US-10-653-048-130	Sequence 130, App
31	49.1	8	16	US-10-340-179-2	Sequence 2, Appli
32	49.1	8	16	US-10-340-179-3	Sequence 3, Appli
33	49.1	9	9	US-09-214-371-37	Sequence 37, Appli
34	49.1	9	9	US-09-214-371-38	Sequence 38, Appli
35	49.1	9	16	US-10-340-179-1	Sequence 1, Appli
36	49.1	11	10	US-09-840-085-31	Sequence 31, Appl
37	49.1	12	9	US-09-214-371-17	Sequence 17, Appl
38	49.1	12	9	US-09-214-371-24	Sequence 24, Appl
39	49.1	12	9	US-09-214-371-25	Sequence 25, Appl
40	49.1	12	12	US-10-609-217-131	Sequence 131, App
41	49.1	12	12	US-10-609-217-132	Sequence 132, App
42	49.1	12	12	US-10-609-217-143	Sequence 143, App
43	49.1	12	12	US-10-609-217-144	Sequence 144, App
44	49.1	12	12	US-10-632-388-131	Sequence 131, App
45	49.1	12	12	US-10-632-388-132	Sequence 132, App

ALIGNMENTS

RESULT 1
US-08-424-550B-252
; Sequence 252, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-252

Query Match      61.8%; Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 FSELWTS 10
Db      1 FSHLWTS 7

RESULT 2
US-09-833-245-1958
; Sequence 1958, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1958
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1958

Query Match      61.8%; Score 34; DB 11; Length 18;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 FSELWTS 10
Db      3 FSEAWTS 9

RESULT 3
US-09-833-245-1959
; Sequence 1959, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1959
; LENGTH: 18

; TELECOMMUNICATION INFORMATION:
; ORGANISM: Homo sapiens
US-09-833-245-1959

Query Match      61.8%; Score 34; DB 11; Length 18;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 FSELWTS 10
Db      3 FSEAWTS 9

RESULT 4
US-09-214-371-35
; Sequence 35, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: PCT/EP97/03549
; PRIOR FILING DATE: 1997-07-04
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: X = Ac-Cys(Acrid)
; NAME/KEY: VARIANT
; LOCATION: (10)
; OTHER INFORMATION: X = Pro-NH2
US-09-214-371-35

Query Match      54.5%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GSPFSELW 8
Db      2 GPTFSDLW 9

RESULT 5
US-09-214-371-36
; Sequence 36, Application US/09214371B
; Patent No. US20010018511A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Picksley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
; FILE REFERENCE: 4-20937/A/PCT
; CURRENT APPLICATION NUMBER: US/09/214,371B
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;/ CURRENT FILING DATE: 1999-03-26
;/ PRIOR APPLICATION NUMBER: PCT/EP97/03549
;/ PRIOR FILING DATE: 1997-07-04
;/ NUMBER OF SEQ ID NOS: 83
;/ SOFTWARE: PatentIn Ver. 2.0

;/ SEQ ID NO 36
;/ LENGTH: 10
;/ TYPE: PRT

;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Description of Artificial Sequence:peptide

;/ NAME/KEY: VARIANT
;/ LOCATION: (1)

;/ OTHER INFORMATION: X = Ac-Cys
;/ NAME/KEY: VARIANT
;/ LOCATION: (10)

;/ OTHER INFORMATION: x = Pro-NH2
;/ US-09-214-371-36

;/

Query Match 54.5%; Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELW 8

DB 2 GPTFSDLW 9

RESULT 6

US-10-221-042-1

;/ Sequence 1, Application US/10221042

;/ Publication No. US20040120946A1

;/ GENERAL INFORMATION:

;/ APPLICANT: KNEKA CORPORATION

;/ TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY

;/ FILE REFERENCE: 12218/5

;/ CURRENT APPLICATION NUMBER: US/10/221,042

;/ CURRENT FILING DATE: 2002-10-09

;/ PRIOR APPLICATION NUMBER: PCT/JP01/03026

;/ PRIOR FILING DATE: 2001-04-09

;/ PRIOR APPLICATION NUMBER: JP 2000-106915

;/ PRIOR FILING DATE: 2000-04-07

;/ NUMBER OF SEQ ID NOS: 13

;/ SOFTWARE: PatentIn version 3.1

;/ SEQ ID NO 1

;/ LENGTH: 13

;/ TYPE: PRT

;/ ORGANISM: Artificial

;/ FEATURE:

;/ OTHER INFORMATION: peptide

;/ NAME/KEY: MISC FEATURE

;/ OTHER INFORMATION: Peptide having a binding affinity for an antibody against

;/ OTHER INFORMATION: betac1-adrenoceptor and/or an antibody against M2 muscarinic recep

;/ US-10-221-042-1

Query Match 54.5%; Score 30; DB 16; Length 13;

Best Local Similarity 85.7%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFFSEL 7

DB 7 GSFFCEL 13

RESULT 7

US-10-155-059-13

;/ Sequence 13, Application US/10155059

;/ Publication No. US20020147173A1

;/ GENERAL INFORMATION:

;/ APPLICANT: Kaelin, William

;/ Jost, Christine

;/ TITLE OF INVENTION: METHODS OF TREATMENT USING
;/ NBS-1, ANTIBODIES AND PROTEINS THEREO, AND USES OF THE
;/ ANTIBODIES

;/ NUMBER OF SEQUENCES: 27

;/ CORRESPONDENCE ADDRESS:

;/ ADDRESSEE: Nixon Peabody LLP

;/ STREET: 101 Federal Street

;/ CITY: Boston

;/ STATE: MA

;/ COUNTRY: USA

;/ ZIP: 02110

;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Diskette

;/ COMPUTER: IBM Compatible

;/ OPERATING SYSTEM: Windows

;/ SOFTWARE: FastSeq for Windows Version 2.0b

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/10/155,059

;/ FILING DATE: 24-May-2002

;/ CLASSIFICATION: <Unknown>

;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: US/09/081,975

;/ FILING DATE: 12-MAY-1998

;/ APPLICATION NUMBER: 60/046,207

;/ FILING DATE: 12-MAY-1997

;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Eisenstein, Ronald I

;/ REGISTRATION NUMBER: 30,628

;/ REFERENCE/DOCKET NUMBER: 47400

;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: 617-345-6054

;/ TELEFAX: 617-345-1300

;/ TELEX: <Unknown>

;/ INFORMATION FOR SEQ ID NO: 13:

;/ SEQUENCE CHARACTERISTICS:

;/ LENGTH: 19 amino acids

;/ TYPE: amino acid

;/ STRANDEDNESS: single

;/ TOPOLOGY: linear

;/ SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-155-059-13

Query Match 54.5%; Score 30; DB 13; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8

DB 8 FSELW 12

RESULT 8

US-10-651-563-53

;/ Sequence 53, Application US/10651563

;/ Publication No. US20040072992A1

;/ GENERAL INFORMATION:

;/ APPLICANT: Sachiko MACHIDA

;/ APPLICANT: Ken TOKUYASU

;/ APPLICANT: Shigeru MATSUNAGA

;/ APPLICANT: Yoshikiyo SAKAKIBARA

;/ APPLICANT: Masuko KOBORI

;/ APPLICANT: Zhesheng WEN

;/ TITLE OF INVENTION: Novel Peptide Capable of Specifically Acting on Biological Membrar

;/ FILE REFERENCE: NF002

;/ CURRENT APPLICATION NUMBER: US/10/651,563

;/ PRIOR FILING DATE: 2003-08-29

;/ PRIOR APPLICATION NUMBER: 2002-253169

;/ PRIOR FILING DATE: 2002-08-30

;/ PRIOR APPLICATION NUMBER: 2003-21198

;/ PRIOR FILING DATE: 2003-01-29

;/ NUMBER OF SEQ ID NOS: 122

;/ SOFTWARE: PatentIn version 3.2

;/ SEQ ID NO 53

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; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic peptide coded by random DNA library
US-10-651-563-53

Query Match          54.5%; Score 30; DB 12; Length 21;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GSPFSELM 8
Db 3 GSPFPLM 10

RESULT 9
US-09-864-761-35636
; Sequence 35636, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35636
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: MAP TO AC009946.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
; OTHER INFORMATION: EST_HUMAN HIT: AW452898.1, EVALUUE 5.00e-03
US-09-864-761-35636

Query Match          54.5%; Score 30; DB 9; Length 22;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FFSLEW 8
Db 5 YFSQLW 10

RESULT 10
US-10-192-381-46
; Sequence 46, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-192-381-46

Query Match          52.7%; Score 29; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ELWTS 10
Db 8 ELWTS 12

RESULT 11
US-10-224-356-36
; Sequence 36, Application US/10224356
; Publication No. US20030144196A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
```



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; TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-356-36

Query Match          52.7%; Score 29; DB 14; Length 16;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELW 8
Db 6 GTRFSEAW 13

RESULT 12
US-10-224-356-17
; Sequence 17, Application US/10224356
; Publication No. US20030144196A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: ACTIVATED T LYMPHOCYTE NUCLEIC ACID SEQUENCES AND POLYPEPTIDES EN
; FILE REFERENCE: D0033 NP
; CURRENT APPLICATION NUMBER: US/10/224,356
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/313,957
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-224-356-17

Query Match          52.7%; Score 29; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSFFSELW 8
Db 4 GTRFSEAW 11

RESULT 13
US-10-372-876-519
; Sequence 519, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 519
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-876-519
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Query Match          52.7%; Score 29; DB 12; Length 21;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 1 GSFFSELW 9
Db 13 GSVYSTINS 21

RESULT 14
US-10-097-065-519
; Sequence 519, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 519
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-097-065-519

Query Match 52.7%; Score 29; DB 14; Length 21;
Best Local Similarity 44.4%; Pred. No. 3.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSPFSELT 9
Db 13 GSVSTIWS 21

RESULT 15

US-09-486-734A-35
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
; FILE REFERENCE: 3339/196048
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: FR 97/10885
; PRIOR FILING DATE: 1997-09-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hsds subunit
US-09-486-734A-35

Query Match 50.9%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSPFSEL 7
Db 2 GSPFKQL 8

Search completed: August 27, 2004, 09:48:10
Job time : 685 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:58 ; Search time 37 Seconds
(without alignments)
25.998 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gffseelwts 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 4494

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	30	54.5	10	C39191	hypothetical prote
2	28	50.9	15	PH1613	Ig H chain V-D-J r
3	25	45.5	12	PT0274	Ig heavy chain CRD
4	24	43.6	7	PH1602	Ig H chain V-D-J r
5	24	43.6	19	S60110	hypothetical prote
6	23	41.8	14	A60622	somatostatin - spo
7	23	41.8	20	A60728	cytochrome P450 3A
8	22	40.0	15	P29501	fibrinopeptide A -
9	22	40.0	16	PH1638	Ig H chain V-D-J r
10	22	40.0	18	S3125	cysteine-rich secr
11	21	38.2	13	PH0138	T-cell receptor be
12	21	38.2	13	I51905	collecting duct wa
13	21	38.2	14	A35105	hypothetical prote
14	21	38.2	16	C37290	homeotic protein G
15	21	38.2	17	PH1331	Ig heavy chain DU
16	21	38.2	19	PH1352	Ig heavy chain DU
17	21	38.2	19	PH1315	Ig heavy chain DU
18	21	38.2	19	S57515	T cell receptor be
19	21	38.2	20	PA0022	protein QAL00011 -
20	21	38.2	20	PH1358	Ig heavy chain DU
21	20	36.4	6	B34835	dnaA protein - Pse
22	20	36.4	10	T13838	cytochrome-c oxida
23	20	36.4	11	S05002	corazonin - Americ
24	20	36.4	13	S32473	lynnadFamide 3 - g
25	20	36.4	13	H56046	urinary tract ston
26	20	36.4	13	PH1620	Ig H chain V-D-J r
27	20	36.4	14	C60414	somatostatin - sli
28	20	36.4	14	B60842	somatostatin I - C
29	20	36.4	14	A60840	somatostatin I - E

30	20	36.4	14	2	S00172	somatostatin I - s
31	20	36.4	14	2	PH1625	Ig H chain V-D-J r
32	20	36.4	14	2	PH1626	Ig H chain V-D-J r
33	20	36.4	14	2	PH1627	Ig H chain V-D-J r
34	20	36.4	14	2	PH1594	Ig H chain V-D-J r
35	20	36.4	15	2	PH1590	Ig H chain V-D-J r
36	20	36.4	15	2	PH1612	Ig H chain V-D-J r
37	20	36.4	16	2	PH1637	Ig H chain V-D-J r
38	20	36.4	17	2	I49593	cystic fibrosis tr
39	20	36.4	17	2	I84733	gene CFTR protein
40	20	36.4	17	2	PH1630	Ig H chain V-D-J r
41	20	36.4	18	2	I40062	shikimate 5-dehydr
42	20	36.4	19	2	S57516	T cell receptor be
43	20	36.4	20	2	PC2347	base nonspecific a
44	20	36.4	20	2	PL0192	Ig lambda 2 chain
45	20	36.4	21	2	PH1731	Ig heavy chain V r

ALIGNMENTS

RESULT 1

C39191
hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C:Species: Bacteroides fragilis
C:Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C:Accession: C39191
R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J. Bacteriol. 173, 176-183, 1991
A:Title: Evidence that a novel tetracycline resistance gene found on two Bacteroides tra
A:Reference number: A39191; MUID:91100280; PMID:1846135
A:Accession: C39191
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <SPE>
A:Cross-references: GB:M37699

Query Match 54.5%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PFSELTWS 10
:|||
Db 2 YFSRPWTS 9

RESULT 2

PH1613
Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1613
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1613
A:Molecule type: DNA
A:Residues: 1-15 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 50.9%; Score 28; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PFSELTW 9
:|:|
Db 9 YFTMLWT 15

RESULT 3

PT0274

```

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0274
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0274
A;Molecule type: DNA
A;Residues: 1-12 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 45.5%; Score 25; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FSELWTS 10
Db . : |||

RESULT 4
PHI602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHI602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PHI580; MUID:93301609; PMID:8315387
A;Accession: PHI602
A;Molecule type: DNA
A;Residues: 1-7 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 43.6%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELWT 9
Db . : |||

RESULT 5
S60110
hypothetical protein - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C;Accession: S60110
R;Thorne, N.M.H.; Hankin, S.; Wilkinson, M.C.; Nunez, C.; Barraclough, R.; McLennan, A.G.
Biochem. J. 311, 717-721, 1995
A;Title: Human diadenosine 5',5','-P(1),P(4)-tetraphosphate pyrophosphohydrolase is a me
A;Reference number: S60110; MUID:96067583; PMID:7487923
A;Accession: S60110
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-19 <THO>
A;Cross-references: EMBL:U30313; NID:gl050959; PIDN:AA050276.1; PID:gl050960

Query Match 43.6%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FSELWTS 10
Db . : |||

RESULT 6
A60622
somatostatin - spotted ratfish
C;Species: Hydrolagus colliei (spotted ratfish)
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C;Accession: A60622
R;Conlon, J.M.
Gen. Comp. Endocrinol. 80, 314-320, 1990
A;Title: [Ser(5)]-somatostatin-14: isolation from the pancreas of a holocephalan fish, t
A;Reference number: A60622; MUID:91160949; PMID:1981569
A;Accession: A60622
A;Molecule type: protein
A;Residues: 1-14 <CON>
C;Superfamily: somatostatin
C;Keywords: hormone; neuropeptide; pancreatic islet
F;3-14/Disulfide bonds: #status experimental

Query Match 41.8%; Score 23; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SFFSELWTS 10
Db ||| : : |||

RESULT 7
A60728
cytochrome P450 3A, troleanomycin-induced - sheep (fragment)
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Ovis sp. (sheep)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-Mar-1999
C;Accession: A60728
R;Pineau, T.; Galtier, P.; Bonfils, C.; Derancourt, J.; Maurel, P.
Biochem. Pharmacol. 39, 901-909, 1990
A;Title: Purification of a sheep liver cytochrome P-450 from the P450IIIA gene subfamily.
A;Reference number: A60728; MUID:90179800; PMID:2310415
A;Accession: A60728
A;Molecule type: protein
A;Residues: 1-20 <PIN>
C;Comment: This cytochrome P450 isozyme is a member of the P450IIIA family but is not fun
C;Genetics:
A;Gene: CYP3A
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: electron transfer; endoplasmic reticulum; heme; monooxygenase; oxidoreductase

Query Match 41.8%; Score 23; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 SFFSELW 8
Db ||| : |||

RESULT 8
F29501
fibrinopeptide A - wombat
C;Species: Vombatidae gen. sp. (wombat)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: F29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: F29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 40.0%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GSFSE 6
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 Db 5 GSFLAE 10

RESULT 9

PH1638
 IG H chain V-D-J region (clone B-less 228) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1638
 R;Jeonsson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Molecule type: DNA
 A:Residues: 1-16 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 40.0%; Score 22; DB 2; Length 16;
 Best Local Similarity 80.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELWT 9
 |||||
 Db 12 SMLWT 16

RESULT 10

S53125
 cysteine-rich secretory protein-3 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
 C:Accession: S53125; S56161
 R;Schwidetzky, U.; Haendler, B.; Schleuning, W.D.
 submitted to the EMBL Data Library, March 1995
 A:Description: Isolation and characterization of the androgen-dependent mouse cysteine-rich secretory protein-3
 A:Reference number: S53125
 A:Accession: S53125
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-18 <SCH>
 A:Cross-references: EMBL:X85321
 R;Schwidetzky, U.; Haendler, B.; Schleuning, W.D.
 Biochem. J. 309, 831-836, 1995
 A:Title: Isolation and characterization of the androgen-dependent mouse cysteine-rich secretory protein-3
 A:Reference number: S56161; MUID:95366959; PMID:7639699
 A:Accession: S56161
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-18 <SC2>
 A:Cross-references: EMBL:X85321

Query Match 40.0%; Score 22; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SPFSE 6
 |||||
 Db 12 SPYSE 16

RESULT 11

PH0138
 T-cell receptor beta chain V-D-J region C8 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
 C:Accession: PH0138
 R;Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richert, J.; Brostoff, S.; Le
 J. Exp. Med. 173, 19-24, 1991

A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context
 A:Reference number: PH0135; MUID:91086843; PMID:1702137
 A:Accession: PH0138
 A:Molecule type: mRNA
 A:Residues: 1-13 <MAR>
 C:Keywords: T-cell receptor

Query Match 38.2%; Score 21; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 9.8e+02;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 FFSLEWTS 10
 |||||
 Db 2 FCASTWTN 9

RESULT 12

I51905
 collecting duct water channel, renal - rat (fragment)
 C:Species: Rattus sp. (rat)
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 07-May-1999
 C:Accession: I51905
 R;Ma, T.; Hasegawa, H.; Skach, W.R.; Frigeri, A.; Verkman, A.S.
 Am. J. Physiol. 266, C189-C197, 1994
 A:Title: Expression, functional analysis, and in situ hybridization of a cloned rat kidney
 A:Reference number: I51905; MUID:94136565; PMID:7508187
 A:Accession: I51905
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-13 <RES>
 A:Cross-references: GB:S68586; NID:9545221
 C:Keywords: kidney

Query Match 38.2%; Score 21; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELWT 9
 |||||
 Db 7 ASLWT 11

RESULT 13

A35105
 hypothetical protein - Neurospora crassa mitochondrion (fragment)
 C:Species: mitochondrion Neurospora crassa
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
 C:Accession: A35105
 R;Saville, B.J.; Collins, R.A.
 Cell 61, 685-696, 1990
 A:Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora mi
 A:Reference number: A35105; MUID:90263093; PMID:2160856
 A:Accession: A35105
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-14 <SAV>
 C:Genetics:
 A:Genome: mitochondrion
 A:Genetic code: SGC3
 C:Keywords: mitochondrion

Query Match 38.2%; Score 21; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELWT 9
 |||||
 Db 2 SPLWT 6

RESULT 14

C37290
 homeotic protein Gsh-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 17-Oct-1997
C;Accession: C37290; C38809
R;Singh, G.; Kaur, S.; Stock, J.L.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Potter
Proc. Natl. Acad. Sci. U.S.A. 88, 10706-10710, 1991
A;Title: Identification of 10 murine homeobox genes.
A;Reference number: A37290; MUID:92073356; PMID:1683707
A;Accession: C37290
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-16 <SIN>
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;1-14/Domain: homeobox homology (fragment) <HOX>

Query Match 38.2%; Score 21; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SFFSEW 8
Db 10 SKPKMW 16

RESULT 15
PH1331
Ig heavy chain DJ region (clone C148-106) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1331
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1331
A;Molecule type: DNA
A;Residues: 1-17 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 38.2%; Score 21; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LWTSS 10
Db 9 VWTSS 12

Search completed: August 27, 2004, 09:23:33
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:59 ; Search time 23 Seconds
(without alignments)
22.639 Million cell updates/sec

Title: AUDET681-1
Perfect score: 55
Sequence: 1 gsfsselslws 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 1457

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	38.2	16	FIBA_EQUAS	P14449 equus asinu
2	20	36.4	11	CORZ_PERAM	P11496 periplaneta
3	20	36.4	13	NP3_LYNSC	P80180 lymanea sta
4	20	36.4	14	SMS1_MYOSC	P20750 myoxocephal
5	20	36.4	14	SMS_ALIMI	P31885 alligator m
6	20	36.4	21	PIL3_ECOLI	P13948 escherichia
7	19	34.5	6	FARP_WONEX	P41966 moniezia ex
8	19	34.5	15	ALB2_TRASC	P81189 trachenys s
9	18	32.7	9	LITR_PHYRO	P08946 phyllomedus
10	18	32.7	10	AKHX_LOCOMI	P81626 locusta mig
11	18	32.7	11	LPW_THETH	P05624 thermus the
12	18	32.7	11	TKNA_SCYCA	P41333 scylorhinu
13	18	32.7	15	FIBA_SYNCA	P14463 syncerus ca
14	18	32.7	16	FIBA_CERSI	P14535 ceratotheri
15	18	32.7	16	FIBA_FELCA	P14450 felis silve
16	18	32.7	16	FIBA_HYLLA	P14453 hylobates l
17	18	32.7	16	FIBA_MACFU	P12803 macaca fusc
18	18	32.7	16	FIBA_MANLE	P14455 mandrillus
19	18	32.7	16	FIBA_ODOHE	P14459 odocoileus
20	18	32.7	16	FIBA_TAPTE	P14536 tapirus ter
21	18	32.7	17	FIBA_PIG	P14460 sus scrofa
22	18	32.7	18	FIBA_CAMDR	P14444 camelus dro
23	18	32.7	18	FIBA_LAMGL	P14454 lama glana
24	18	32.7	18	TOP1_KLEAE	P46155 klebsiella
25	18	32.7	19	FIBA_BISBO	P14441 bison bonas
26	18	32.7	19	FIBA_BUBBU	P14442 bubalus bub
27	18	32.7	19	FIBA_MUNMU	P14457 muntiacus m
28	18	32.7	19	FIBA_SHEEP	P14451 ovitis aries
29	18	32.7	23	PQQA_PSEAB	Q92aa0 pseudomonas
30	18	32.7	23	PQQA_PSEAB	Q86qv4 pseudomonas
31	18	32.7	23	PQQA_PSEAB	Q919ul pseudomonas
32	17.5	31.8	8	LCKS_LEUMA	P19987 leucophaea
33	17	30.9	8	HTF1_PERAM	P04548 periplaneta

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34 17 30.9 8 1 HTF_TENMO
35 17 30.9 10 1 HTF_HELZE
36 17 30.9 10 1 LABA_JATMU
37 17 30.9 11 1 MBBI_KLEPN
38 17 30.9 17 1 UP41_UPEIN
39 17 30.9 20 1 CRTC_SPTOL
40 17 30.9 20 1 GBB4_RAT
41 17 30.9 20 1 LPP3_HUMAN
42 17 30.9 21 1 NDK_CANAL
43 17 30.9 22 1 LANM_STRMU
44 17 30.9 23 1 IAPP_LBPEU
45 17 30.9 23 1 PRO3_DACGL

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ALIGNMENTS

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RESULT 1
FIBA_EQUAS
AC P14449; STANDARD; PRT; 16 AA.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

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Query Match 38.2%; Score 21; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 GSFSE 6
Db 6 GEFISE 11

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RESULT 2
CORZ_PERAM
ID CORZ_PERAM STANDARD; PRT; 11 AA.
AC P11496;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Corazonin.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.

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RC TISSUE=Corpora cardiaca;
RX MEDLINE=89325572; PubMed=2753132;
RA Veenstra J.A.;
RT "Isolation and structure of corazonin, a cardioactive peptide from
RT the American cockroach.";
RL FEBS Lett. 250:231-234(1989).
CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
CC in the physiological regulation of the heart beat.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; S05002; S05002.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 36.4%; Score 20; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 7.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 FSELWTS 10
:| | |
Db 5 YSRGWTN 11

RESULT 3
NP3 LYMST
ID -NP3 LYMST STANDARD; PRT; 13 AA.
AC P80180;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lyman-DP-amide 3.
OS Lymanaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Bascommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnsen A.H., Rehfeld J.F.;
RT "LymnaeDFamides, a new family of neuropeptides from the pond snail,
RT Lymanaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates.";
RL Eur. J. Biochem. 213:875-879(1993).
CC -!- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
DR PIR; S32473; S32473.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13 AMIDATION.
FT UNSURE 12 12
SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 36.4%; Score 20; DB 1; Length 13;
Best Local Similarity 46.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSFPSE 6
:| | |
Db 7 GSATSD 12

RESULT 4
SMS1 MYOSC
ID -SMS1 MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin 1.
OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
OS Oncorhynchus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M.scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
RT prosomatostatins I and II isolated from the pancreatic islets of two
RT species of teleostean fish: the daddy sculpin and the flounder.";
RL Eur. J. Biochem. 168:647-652(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=O.kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plisetkaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorbman A.;
RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
RT somatostatins";
RL Gen. Comp. Endocrinol. 63:252-263(1986).
RN [3]
RP SEQUENCE.
RC SPECIES=A.anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
RT structural features from the European eel (Anguilla anguilla).";
RL Gen. Comp. Endocrinol. 72:181-189(1988).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR; A60840; A60840.
DR PIR; B60842; B60842.
DR PIR; S00172; S00172.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Hormone; Multigene family.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 36.4%; Score 20; DB 1; Length 14;
Best Local Similarity 44.4%; Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SFFSELWTS 10
:| | | |
Db 5 NFFWKTFTS 13

RESULT 5
SMS ALLMI
ID -SMS ALLMI STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (pseudemys scripta);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496, 34903;
RN [1]
RP SEQUENCE.
RC SPECIES=A.mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RT and stomach of the alligator.";
RL Peptides 14:573-579(1993).
RN [2]

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RP SEQUENCE.
RC SPECIES=T.scrypta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
RT somatostatin from the turtle, Pseudemys scripta.";
RL Peptides 11:461-466(1990).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR: C60414; C60414. Somatostatin.
DR InterPro: IPR004250; Somatostatin.
DR Pfam: PF03002; Somatostatin; 1.
KW Hormone.
FT DISULFID 3 14 BY SIMILARITY.
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 36.4%; Score 20; DB 1; Length 14;
Best Local Similarity 44.4%; Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SPFSLEWTS 10
Db :||:
5 NFFWKFTFS 13

RESULT 6
PIL3 ECOLI STANDARD; PRT; 21 AA.
AC P13948;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Fimbrial protein precursor (Pilin) (Fragment).
GN TRAA.
OS Escherichia coli.
OG Plasmid ColB4-K98.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87008371; PubMed=3531163;
RA Finlay B.B., Frost L.S., Paranchych W.;
RT "Origin of transfer of IncF plasmids and nucleotide sequences of the
RT type II oriT, traM, and traY alleles from ColB4-K98 and the type IV
RT traY allele from R100-1.";
RL J. Bacteriol. 168:132-139(1986).
CC -!- FUNCTION: PROFILIN IS THE PRECURSOR OF THE SEXFILUS SUBUNIT. THE
CC SEXFILUS ARE FILAMENTOUS SURFACE APPENDAGES REQUIRED FOR CELL-TO-
CC CELL CONTACT DURING BACTERIAL CONJUGATION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC -----
DR EMBL: M15135; AAB04666.1; -.
DR InterPro: IPR008873; TraA.
DR Pfam: PF05513; TraA; 1.
KW Plasmid; Conjugation; Fimbria.
FT PROPEP 1 >21
FT NON TER 21 21
SQ SEQUENCE 21 AA; 2198 MW; 076C0D0C5E9D14EA CRC64;

Query Match 36.4%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 SPFS 5
Db :|||
18 SPFS 21

RESULT 7
FARP_MONEK STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRamide-like neuropeptide GNFRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFamide: a novel FMRamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR PIR: A43129; A43129.
KW Neuropeptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 34.5%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFF 4
Db :|||
1 GNFF 4

RESULT 8
ALB2 TRASC STANDARD; PRT; 15 AA.
AC P81189;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 68 kDa serum albumin (Alb-2) (Fragment).
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX NCBI_TaxID=34903;
RN [1]
RP SEQUENCE.
RX MEDLINE=98103404; PubMed=9440230;
RA Brown M.A.; Chambers G.K., Licht P.;
RT "Purification and partial amino acid sequences of two distinct
RT albumins from turtle plasma.";
RL Comp. Biochem. Physiol. 118B:367-374(1997).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- MISCELLANEOUS: In the red-eared slider turtle, there are two forms
CC of albumin, ALB-1 and ALB-2.
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
DR InterPro: IPR000264; Serum albumin.
DR PROSITE: PS00212; ALBUMIN; PARTIAL.
KW Metal-binding; Lipid-binding.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1733 MW; 4B7422B89FF73223 CRC64;

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Query Match      34.5%; Score 19; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GSFSEL 7
DB 9 GHXFEL 15

RESULT 9
LITR_PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rhodai-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA "Erspamer V.;
RT "Rhodai-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
family.
DR PIR; S07241; S07241.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1090 MW; 4ECCLEB61ADC377 CRC64;

Query Match      32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 ELWTS 10
DB 1 QLWAT 5

RESULT 10
AKHX_LOCMI STANDARD; PRT; 10 AA.
AC P81626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Sievert K.J.;
RL Submitted (DEC-1998) to Swiss-Prot.
CC -1- FUNCTION: Probably involved in the regulation of locust
intermediary metabolism, behavior and/or development.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match      32.7%; Score 18; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FSELWT 9
DB 4 FSRDWS 9

RESULT 11
LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
HB8 trpE and trpG.";
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
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CC EMBL; X07744; CAA30565.1; -.
DR Tryptophan biosynthesis; Leader peptide.
KW SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match      32.7%; Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SELW 8
DB 5 SALW 8

RESULT 12
TKNA_SCYCA STANDARD; PRT; 11 AA.
AC P41333;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyllorhinidae; Scyllorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 RT peptides from the brain of the dogfish, *Scyllorhinus canicula*.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S33300; S33300.
 DR InterPro; IPR002040; Tachy Neurokinin.
 DR PROSITE; PS00267; TACHYKININ_1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;
 Query Match 32.7%; Score 18; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GSFF 4
 Db | | |
 5 GQFF 8
 RESULT 13
 FIBA SYNCA
 ID FIBA SYNCA STANDARD; PRT; 15 AA.
 AC P14463;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Syncerus caffer (Cape buffalo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Syncerus.
 OX NCBI_TaxID=9970;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=67209145; PubMed=6033721;
 RA Doolittle R.F., Schubert D., Schwartz S.A.;
 RT "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
 RT Dromedary camel, mule deer, and cape buffalo.";
 RL Arch. Biochem. Biophys. 118:456-467(1967).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 15
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1480 MW; 4E998EA5F0B41CC6 CRC64;
 Query Match 32.7%; Score 18; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSPPSE 6
 Db | | |
 5 GEFLAE 10
 RESULT 14
 FIBA CERSI
 ID FIBA CERSI STANDARD; PRT; 16 AA.
 AC P14535;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 OX NCBI_TaxID=9807;
 RN [1]
 RP SEQUENCE.
 RA O'Neill P.B., Doolittle R.F.;
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
 RL Syst. Zool. 22:590-595(1973).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1639 MW; 0958CBB6293F4C81 CRC64;
 Query Match 32.7%; Score 18; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GSPPSE 6
 Db | | |
 6 GDFIAE 11
 RESULT 15
 FIBA FELCA
 ID FIBA FELCA STANDARD; PRT; 16 AA.
 AC P14450;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.

KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1620 MW; C3C98EB62D6CC7D3 CRC64;
 Query Match 32.7%; Score 18; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GSPFSE 6
 Db 6 GEFIAE 11

Search completed: August 27, 2004, 09:26:09
 Job time : 26 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 09:19:59 ; Search time 112 Seconds

(without alignments)
28.171 Million cell updates/sec

Title: AUDET681-1

Perfect score: 55

Sequence: 1 gsfselelws 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 9533

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	18	Q8HK12	Q8HK12 apomomma co
2	24	43.6	11	Q77895	Q77895 oreochromis
3	24	43.6	11	Q77896	Q77896 oreochromis
4	24	43.6	22	Q9W6D7	Q9W6D7 gallus gall
5	24	43.6	23	Q9TRC6	Q9TRC6 canis famill
6	23	41.8	11	P8J537	P8J537 lactobacill
7	23	41.8	13	Q9XLI2	Q9XLI2 bemisia tab
8	23	41.8	15	Q9R5D6	Q9R5D6 chromidum
9	23	41.8	16	Q8QGAI	Q8QGAI brachydanio
10	23	41.8	20	Q96T45	Q96T45 homo sapien
11	23	41.8	22	Q93346	Q93346 human herpe
12	22	40.0	12	Q9TRT7	Q9TRT7 bos taurus
13	22	40.0	16	Q9TR88	Q9TR88 bos taurus
14	22	40.0	17	Q7Y1X8	Q7Y1X8 lilium long
15	22	40.0	18	Q8HKH6	Q8HKH6 apomomma un
16	22	40.0	18	Q9S8I7	Q9S8I7 oryza sativ

17	22	40.0	18	10	Q9S8I8	Q9S8I8 oryza sativ
18	21	38.2	9	4	Q9S953	Q9S953 homo sapien
19	21	38.2	13	11	Q80Y03	Q80Y03 rattus sp.
20	21	38.2	16	2	Q9R4F2	Q9R4F2 streptomyce
21	21	38.2	16	11	Q9QW76	Q9QW76 mus sp. hom
22	21	38.2	17	10	Q9S7E8	Q9S7E8 arabidopsis
23	21	38.2	18	10	Q9S7E5	Q9S7E5 arabidopsis
24	21	38.2	19	2	Q53311	Q53311 streptococ
25	21	38.2	20	6	Q95MK5	Q95MK5 varecia var
26	21	38.2	20	12	Q65548	Q65548 human herpe
27	21	38.2	22	8	Q94XD4	Q94XD4 pteroxanum
28	21	38.2	23	11	Q8CB74	Q8CB74 mus musculu
29	21	38.2	23	12	Q86127	Q86127 vesicular s
30	20.5	37.3	21	2	Q9L4S9	Q9L4S9 salmonella
31	20.5	37.3	23	13	Q8JHU5	Q8JHU5 gallus gall
32	20	36.4	10	8	P92576	P92576 bipes bipor
33	20	36.4	11	7	Q77898	Q77898 oreochromis
34	20	36.4	11	7	Q77894	Q77894 oreochromis
35	20	36.4	12	6	Q46664	Q46664 macropus ro
36	20	36.4	12	11	Q61331	Q61331 mus musculu
37	20	36.4	13	11	Q7TMB4	Q7TMB4 mus musculu
38	20	36.4	15	4	Q16297	Q16297 homo sapien
39	20	36.4	15	13	Q8AXQ9	Q8AXQ9 xenopus lae
40	20	36.4	16	9	O21922	O21922 streptococ
41	20	36.4	16	11	Q9Z0J2	Q9Z0J2 mus musculu
42	20	36.4	17	6	Q7YR63	Q7YR63 macaca neme
43	20	36.4	17	13	Q9DFB5	Q9DFB5 brachydanio
44	20	36.4	18	4	Q8N0X8	Q8N0X8 homo sapien
45	20	36.4	18	6	P82674	P82674 bos taurus

ALIGNMENTS

RESULT 1

Q8HK12

ID Q8HK12 PRELIMINARY; PRT; 18 AA.

AC Q8HK12; 01-MAR-2003 (TRENBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE NADH dehydrogenase subunit 1 (Fragment).

GN ND1.

OS Aponomma concolor (schidna tick).

OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Parasitiformes; Ixodida; Ixodidae; Aponomma.

OX NCBI_TaxID=65640;

RN [1]_TaxID=65640;

RP SEQUENCE FROM N.A.

RA Campbell N.J.H., Murrell A., Barker S.C.;

RT "The value of idiosyncratic markers and conserved tRNA sequences from

the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for

phylogenetic inference."

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY059185; AAL79389.1; -

DR GO; GO:0005739; C:mitochondrion; IEA.

FW Mitochondrion.

KT NON TER 1

SQ SEQUENCE 18 AA; 2241 MW; E50D0DD0446AD639 CRC64;

Query Match 47.3%; Score 26; DB 8; Length 18;

Best Local Similarity 55.6%; Pred. No. Se+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SPFSELELWS 10

Db 10 SFCINFWTS 18

RESULT 2

O77895

ID O77895 PRELIMINARY; PRT; 11 AA.

AT 077895;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050005; AAC41344.1; --
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;

Query Match 43.6%; Score 24; DB 7; Length 11;
 Best Local Similarity 50.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FFSLEWTS 10
 DB 3 FWSILWVA 10

RESULT 3
 O77896 PRELIMINARY; PRT; 11 AA.
 ID 077896
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050006; AAC41345.1; --
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match 43.6%; Score 24; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 7.2e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FFSLEW 8
 DB 3 FWSMLW 8

RESULT 4
 Q9W6D7 PRELIMINARY; PRT; 22 AA.
 ID Q9W6D7
 AC Q9W6D7;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hydroxyindole-o-methyltransferase isoform A (fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99067015; PubMed=9851690;
 RA Grechez-Cassiau A., Bernard M., Ladjali K., Rodriguez I.R., Voisin P.;
 RT "Structural analysis of the chicken hydroxyindole-O-methyltransferase
 gene.";
 RL Eur. J. Biochem. 258:44-52(1998).
 DR EMBL; AF116455; AAD23444.1; --
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Methyltransferase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 22 22
 SQ SEQUENCE 22 AA; 2783 MW; 35726EABF1E450C8 CRC64;

Query Match 43.6%; Score 24; DB 13; Length 22;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 FSELW 8
 DB 12 FADLW 16

RESULT 5
 Q9TRC6 PRELIMINARY; PRT; 23 AA.
 ID Q9TRC6
 AC Q9TRC6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Cytochrome P450 DBP-1 isoform (fragment).
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94198820; PubMed=8185738;
 RA Shiraga T., Iwasaki K., Nozaki K., Tamura T., Yamazoe Y., Kato R.,
 RA Takahashi A.;
 RT "Isolation and characterization of four cytochrome P450 isozymes from
 untreated and phenobarbital-treated beagle dogs.";
 RL Biol. Pharm. Bull. 17:22-28(1994).
 SQ SEQUENCE 23 AA; 2638 MW; AF868888F8029F8 CRC64;

Query Match 43.6%; Score 24; DB 6; Length 23;
 Best Local Similarity 57.1%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 SPFSELW 8
 DB 6 SPXGETW 12

RESULT 6
 P83537 PRELIMINARY; PRT; 11 AA.
 ID P83537
 AC P83537;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Unknown protein from 2D-page (fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RA Drews O., Welss W., Reil G., Parlar H., Wait R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -I- INDUCTION: BY ELEVATED HYDROSTATIC PRESSURE.
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
 CC PROTEIN IS: 65 KDA.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;

Query Match 41.8%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSFFS 5
 Db 1 GSFFA 5

RESULT 7
 Q9XLI2 PRELIMINARY; PRT; 13 AA.
 ID O9XLI2
 AC O9XLI2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase I (Fragment).
 OS Bemisia tabaci (Sweetpotato whitefly).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;
 OC Aleyrodidae; Aleyrodinae; Bemisia.
 OX NCBI_TaxID=7038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=10583831;
 RA Frohlich D.R., Torres-Jerez I., Bedford I.D., Markham P.G.,
 Brown J.K.;
 RT "A phylogeographical analysis of the Bemisia tabaci species complex
 based on mitochondrial DNA markers.";
 RL Mol. Ecol. 8:1683-1691(1999).
 DR EMBL; AF110703; AAD28415.1;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1639 MW; 8DD68729F5744365 CRC64;

Query Match 41.8%; Score 23; DB 8; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SPFFSELW 8
 Db 1 SYFTSSW 7

RESULT 8
 Q9R5D6 PRELIMINARY; PRT; 15 AA.
 ID Q9R5D6
 AC Q9R5D6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 41 kDa protein
 DE (Fragment).
 OS Chromatium vinosum.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 OC Chromatiaceae; Allochromatium.
 OX NCBI_TaxID=1049;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=931146381; PubMed=1490603;
 RA Liebergessel M., Schmidt B., Steinbuechel A.;
 RT "Isolation and identification of granule-associated proteins relevant
 for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum
 D.";
 RL FEMS Microbiol. Lett. 78:227-232(1992).
 SQ SEQUENCE 15 AA; 1874 MW; 165FA9A16BCA2A9D CRC64;

Query Match 41.8%; Score 23; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1.5e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SPFFSELW 8
 Db 5 NFFENDW 11

RESULT 9
 Q8QGA1 PRELIMINARY; PRT; 16 AA.
 ID Q8QGA1
 AC Q8QGA1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Insulin-like growth factor-1b (Fragment).
 GN IGF1B.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21261964; PubMed=11368902;
 RA Chen M.H.C., Lin G.H., Gong H.Y., Weng C.F., Chang C., Wu J.L.;
 RT "The characterization of prepro-insulin-like growth factor-1 Ea-2
 expression and insulin-like growth factor-1 genes (devoid 81 bp) in
 the zebrafish (Danio rerio).";
 RL Gene 268:67-75(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gong H.Y., Hu M.C., Chen M.H.C., Chen M.C., Weng C.F., Lin C.J.F.,
 Lin G.H., Wu J.L.;
 RT "Developmental expression of zebrafish HNF1g, a novel hepatocyte
 nuclear factor-1 in zebrafish pronephros formation.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF486298; AAL92052.1;
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1913 MW; 1D0A5A4F917EE868 CRC64;

Query Match 41.8%; Score 23; DB 13; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GSFFSELW 8
 Db 4 GHFFQHW 11

RESULT 10
 Q96T45 PRELIMINARY; PRT; 20 AA.
 ID Q96T45
 AC Q96T45;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE MER receptor tyrosine kinase (Fragment).
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20517330; PubMed=11062461;
RA Gal A., Li Y., Thompson D.A., Weir J., Orth U., Jacobson S.G.,
RA Apfelstedt-Sylla E., Vollrath D.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF366903; AAK54121.1;
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Kinase; Receptor.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2332 MW; A853B8F7E8CE2910 CRC64;

Query Match 41.8%; Score 23; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GSPFSELM 8
DB 11 GULPALM 18

RESULT 11
Q69346 PRELIMINARY; PRT; 22 AA.
AC Q69346;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 34K protein (Fragment).
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17;
RX MEDLINE=87010565; PubMed=3020164;
RA Davison B.A.J., Scott J.B.;
RT "DNA Sequence of the Major Capsid Protein Gene of Herpes Simplex Virus."
RL J. Gen. Virol. 67:2279-2286(1986).
DR EMBL; X04467; CAA28153.1;
DR GO; GO:0013067; P:virial assembly, maturation, egress, and rel. .; IEA.
DR InterPro; IPR007629; Herpes_UL20.
DR Pfam; PF04544; Herpes_UL20; 1.
FT NON TER 1 1
SQ SEQUENCE 22 AA; 2484 MW; 2CBA431B3E4C1A0B CRC64;

Query Match 41.8%; Score 23; DB 12; Length 22;
Best Local Similarity 42.9%; Pred. No. 2.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 FFESELM 9
DB 6 FLAEFT 12

RESULT 12
Q9TRT7 PRELIMINARY; PRT; 12 AA.
AC Q9TRT7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 15 kDa amyloid protein A homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92132498; PubMed=1734497;
RA Veiby O.P., Sletten K., Husby G., Nordstoga K.;
RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils of bovine kidney."
RL Scand. J. Immunol. 35:63-69(1992).
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1503 MW; 64CDB543C6DB4AEB CRC64;

Query Match 40.0%; Score 22; DB 6; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SFFSELM 8
DB 1 SFFEXY 7

RESULT 13
Q9TR88 PRELIMINARY; PRT; 16 AA.
AC Q9TR88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PA28 protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=95081084; PubMed=7989312;
RA Mott J.D., Pramanik B.C., Moomaw C.R., Afendis S.J., DeMartino G.N.,
RA Slaughter C.A.;
RT "PA28, an activator of the 20 S proteasome, is composed of two nonidentical but homologous subunits."
RL J. Biol. Chem. 269:31466-31471(1994).
DR GO; GO:0008537; C:proteasome activator complex; IEA.
DR GO; GO:0008538; F:proteasome activator activity; IEA.
DR InterPro; IPR003186; PA28_beta.
DR Pfam; PF02252; PA28_beta; 1.
FT NON TER 1 1
SQ SEQUENCE 16 AA; 1898 MW; 126D340D14EE9BDE CRC64;

Query Match 40.0%; Score 22; DB 6; Length 16;
Best Local Similarity 42.9%; Pred. No. 2.5e+03;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 SFFSELM 8
DB 1 AFYAEV 7

RESULT 14
Q7YIX8 PRELIMINARY; PRT; 17 AA.
AC Q7YIX8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Male gametic cell-specific (Fragment).
GN LGC1.

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OS Liliu longifloru (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Liliu.
 ON NCBI_TaxID=4690;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=22615576; PubMed=12729896;
 RA Singh M., Bhalla P.L., Xu H., Singh M.B.;
 RT "Isolation and characterization of a flowering plant male gametic
 cell-specific promoter(1).";
 RL FEBS Lett. 542:47-52(2003).
 DR EMBL; AY207012; AAP37155.1; -.
 FT NON TER 17
 SQ SEQUENCE 17 AA; 1880 MW; 661B63484969679F CRC64;

Query Match 40.0%; Score 22; DB 10; Length 17;
 Best Local Similarity 60.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 FSELW 8
 |||:
 Db 11 FSSVW 15

RESULT 15

Q8HKH6 PRELIMINARY; PRT; 18 AA.
 AC Q8HKH6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN ND1.
 OS Aponomma undatum (goanna tick).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Aponomma.
 ON NCBI_TaxID=65642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Campbell N.J.H., Murrell A., Barker S.C.;
 RT "The value of idiosyncratic markers and conserved tRNA sequences from
 the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for
 phylogenetic inference.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059193; AAL79395.1; ...
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 2362 MW; 1AE724D04CC8D631 CRC64;

Query Match 40.0%; Score 22; DB 8; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 SPFSELWT 9
 |||
 Db 10 SPCINFWT 17

Search completed: August 27, 2004, 09:28:10
 Job time : 118 secs

B/ANK